

Fig.1.

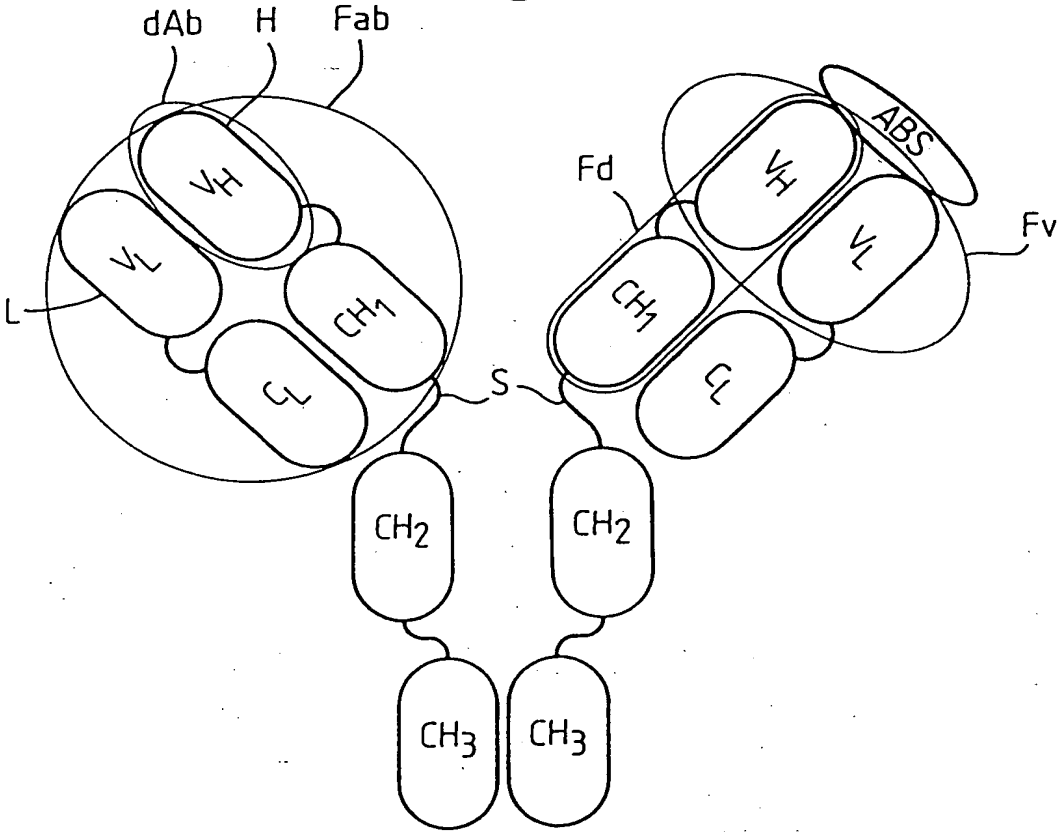


Fig.2 a

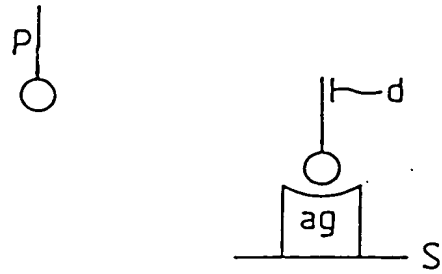


Fig.2 b

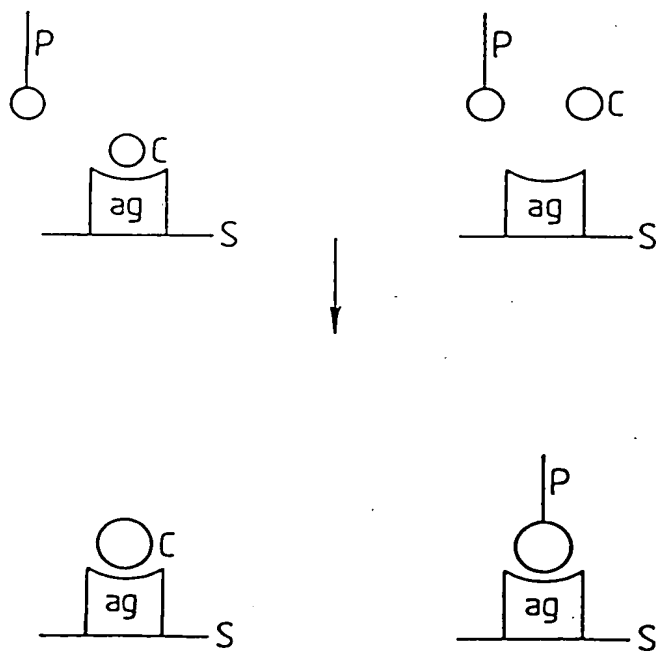
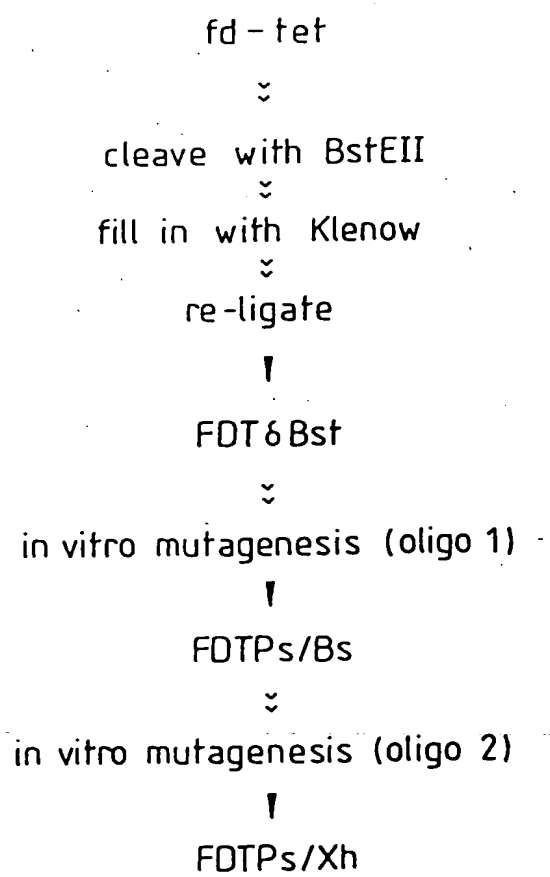


Fig. 3.



(1653)
 ACA ACT TTC AAC AGT TGA GGA GAC GGT GAC CGT AAG CTT CTG CAG TTG GAC CTG AGC (SEQ ID NO. 177)
 GGA GTG AGA ATA (1620)
 (1653)
 ACA ACT TTC AAC AGT TTC CCG TTT GAT CTC GAG CTC CTG CAG TTG GAC CTG (SEQ ID NO. 178)
 (1704)
 GTC GTC TTT CCA GAC GTT AGT (SEQ ID NO. 179)

Fig.4 a

GENE III

GENE IIII

SIGNAL
CLEAVAGE SITE

Fig.4 b

(1624)
 A TCT CAC TCC GCT (1650)
 GAA ACT GTT GAA AGT (SEQ ID NO. 180)
 Q V Q L Q (SEQ ID NO. 1) V T V S S (SEQ ID NO. 2)
 B TCT CAC TCC GCT CAG GTC CAA CTG CAG AAG CTT ACG GTC ACC GTC TCC TCA ACT GTT GAA AGT (SEQ ID NO. 181)
 PstI BstEII
 Q V Q L Q (SEQ ID NO. 1) L E I K R (SEQ ID NO. 3)
 C TCT CAC TCC GCT CAG GTC CAA CTG CAG GAG CTC GAG ATC AAA CGG GAA ACT GTT GAA AGT (SEQ ID NO. 182)
 PstI XhoI

Fig.5a

rbs M K Y L L P T A A
 GCATGCAAATTCTATTTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCC
 10 20 30 40 50 60
 SphI
 PelB leader
 A G L L L L A A O P A M A Q V Q L Q E S
 GCTGGATTGTTATTACTCGCTGCCCAACCAGCGATGGCCCAGGTGCAGCTGCAGGAGTCA
 70 80 90 100 110 120
 PstI
 G P G L V A P S Q S L S I T C T V S G F
 GGACCTGGCCTGGTGGCGCCCTCACAGAGCCTGTCCATCACATGCACCGTCTCAGGGTTC
 130 140 150 160 170 180
 S L T G Y G V N W V R Q P P G K G L E W
 TCATTAACCGGCTATGGTGTAAACTGGGTTCGCCAGCCTCCAGGAAAGGGTCTCGAGTGG
 190 200 210 220 230 240
 VHD1.3
 L G M I W G D G N T D Y N S A L K S R L
 CTGGAATGATTTGGGGTGATGGAAACACAGACTATAATTCAGCTCTCAAATCCAGACTG
 250 260 270 280 290 300
 S I S K D N S K S Q V F L K M N S L H T
 AGCATCAGCAAGGACAACCTCCAAGAGCCAAGTTTCTTAAAAATGAACAGTCTGCACACT
 310 320 330 340 350 360
 D D T A R Y Y C A R E R D Y R L D Y W G
 GATGACACAGCCAGGTACTACTGTGCCAGAGAGAGAGATTATAGGCTTGACTACTGGGGC
 370 380 390 400 410 420
 Linker Peptide
 Q G T T V T V S S G G G G S G G G S G
 CAAGGCACCAACGGTCAACCGTCTCCTCaggtggaggcgggttcaggcggaggtggctcgggc
 430 440 450 460 470 480
 BstEII
 G G G S D I E L T Q S P A S L S A S V G
 ggtggcggatcgGACATCGAGCTCACTCAGTCTCCAGCCTCCCTTTCTGCGTCTGTGGGA
 490 500 510 520 530 540
 SacI

Fig.5 b

E T V T I T C R A S G N I H N Y L A W Y
GAAACTGTCACCATCACATGTCGAGCAAGTGGGAATATTCACAATTATTTAGCATGGTAT
550 560 570 580 590 600

Q Q K Q G K S P Q L L V Y Y T T T L A D
CAGCAGAAACAGGGAAAATCTCCTCAGCTCCTGGTCTATTATACAACAACCTTAGCAGAT
610 620 630 640 650 660

VKD1.3

G V P S R F S G S G S G T Q Y S L K I N
GGTGTGCCATCAAGGTTTCAGTGGCAGTGGATCAGGAACACAATATTCTCTCAAGATCAAC
670 680 690 700 710 720

S L Q P E D F G S Y Y C Q H F W S T P R
AGCCTGCAACCTGAAGATTTTGGGAGTTATTACTGTCAACATTTTGGGAGTACTCCTCGG
730 740 750 760 770 780

Myc Tag (TAG1)

T F G G G T K L E I K R E O K L I S E E
ACGTTCCGGTGGAGGGACCAAGCTCGAGATCAAACGGGAACAAAACTCATCTCAGAAGAG
790 800 810 820 830 840

XhoI

D L N * * (SEQ ID NO. 183)

GATCTGAATTAATAATGATCAAACGGTAATAAGGATCCAGCTCGAATTC (SEQ ID NO. 184)
850 860 870 880

EcoRI

Fig.6.

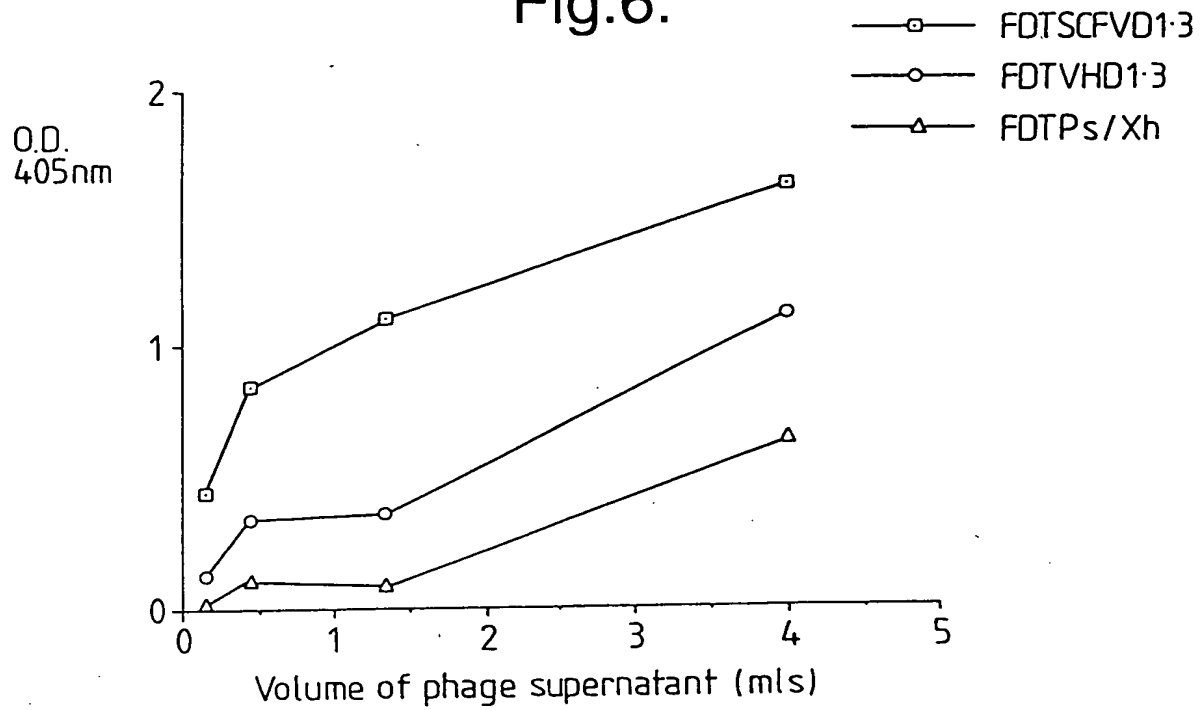


Fig.7.

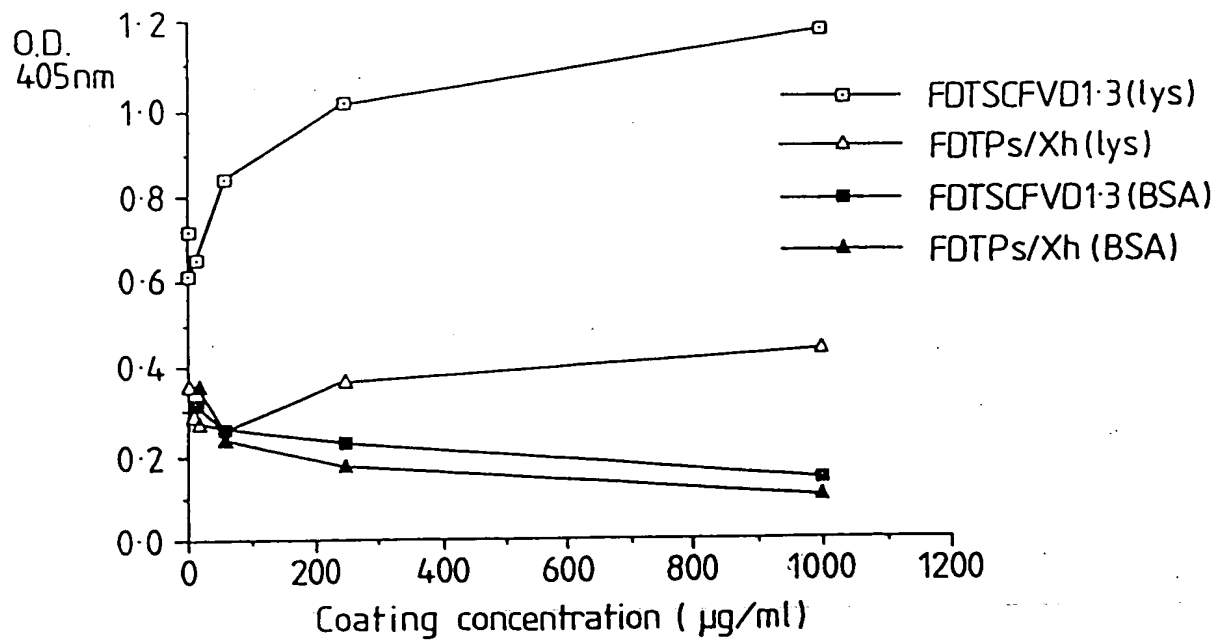


Fig.8.

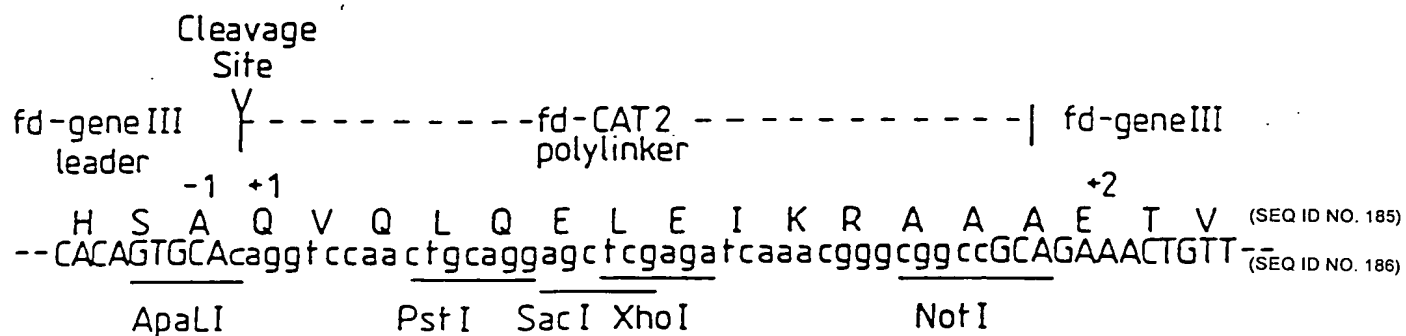


Fig.9.

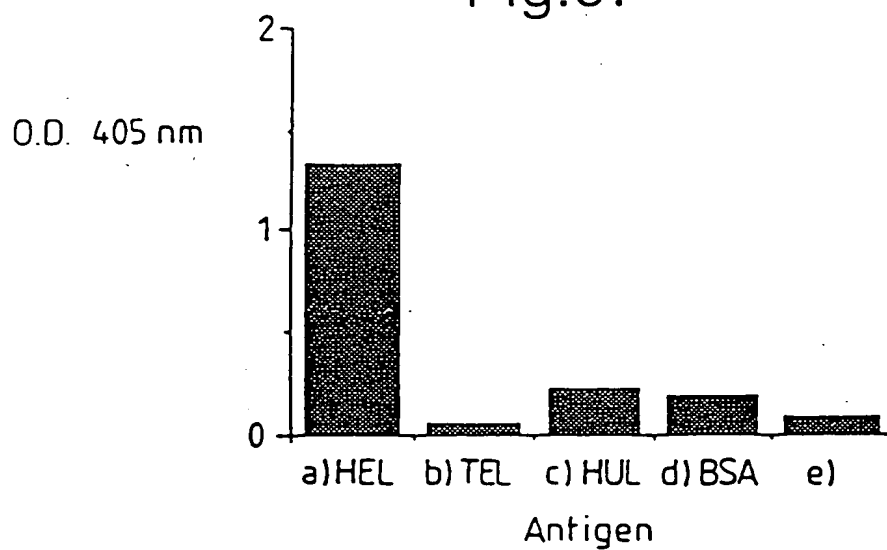


Fig.10a

M K Y L L P T A A
GCATGCAAATTCTATTTCAAGGAGACAGTCATAATGAAATACCTATTGCCTAGGGCAGCC
10 20 30 40 50 60

A G L L L L A A Q P A M A Q V Q L Q E S
GCTGGATTGTTATTACTGCTGCCCAACCAGCGATGGCCCTGGTGCAGCTGCAGGAGTCA
70 80 90 100 110 120

G P G L V A P S Q S L S I T C T V S G F
GGACCTGGCCCTGGTGGGGCCCTCAGAGCCGTGCCATCACATGCACCGTCTCAGGGTTC
130 140 150 160 170 180

S L T G Y G V N W V R Q P P G K G L E W
TCATTAAACCGGCTATGGTGTAAACTGGGTTCCGCCAGCCTCCAGGAAAGGGTCTCGAGTGG
190 200 210 220 230 240

L G M I W G D G N T D Y N S A L K S R L
CTGGGAATGATTTGGGGTGATGGAAACACAGACTATAATTTCAGCTCTCAAATCCAGACTG
250 260 270 280 290 300

S I S K D N S K S Q V F L K M N S L H T
AGCATCAGCAAGGACAACCTCCAAGAGCCAAGTTTTCTTAAAAATGAACAGTCTGCACACT
310 320 330 340 350 360

D D T A R Y Y C A R E R D Y R L D Y W G
GATGACACAGCCAGGTACTACTGTGCCAGAGAGAGAGATTATAGGCTTGACTACTGGGGC
370 380 390 400 410 420

Q G T T V T V S S A S T K G P S V F P L
CAAGGCACCAAGGTACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTG
430 440 450 460 470 480

A P S S K S T S G G T A A L G C L V K D
GCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGGGCCCTGGGCTGCCTGGTCAAGGAC
490 500 510 520 530 540

Fig.10b

Y F P E P V T V S W N S G A L T S G V H
TACTTCCCCGAACCGGTGACGGTGTCTGTGGAAGTCAAGGCGCCCTGACCCAGCGGGGTGCAC
550 560 570 580 590 600

T F P A V L Q S S G L Y S L S S V V T V
ACCTTCCCGGCTGTCTTACAGTCTCTAGGACTCTACTCCCTCAGCAGGTGGTGACCGTG
610 620 630 640 650 660

P S S S L G T Q T Y I C N V N H K P S N
CCCTCCAGCAGCTTGGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAAC
670 680 690 700 710 720

T K V D K K V E P K S S * * (SEQ ID NO. 187)
ACCAAGGTGACACAAGAACTTGAAGCCAAATCTTCATAATAACCCGGGAGCTTGCATGCA
730 740 750 760 770 780

M K Y L L P T A A A G L
AATTCTATTTCAGGAGACAGTTCATAATGAATACCTATTGCCTACGGCAGCCGCTGGAT
790 800 810 820 830 840

L L L A A Q P A M A D I E L T Q S P A S
TGTTATTACTCGCTGCCCCAACCCAGCGATGGCCGACATCGAGCTCACCCAGTCTCCAGCCT
850 860 870 880 890 900

L S A S V G E T V T I T C R A S G N I H
CCCTTTCTGGTCTGTGCGGAGAACTGTACCATCACATGTGCGAGCAAGTGGGAATATT
910 920 930 940 950 960

N Y L A W Y Q Q K Q G K S P Q L L V Y Y
ACAATTATTTAGCATGGTATCAGCAGAAACAGGGAAATCTCCTCAGCTCCTGGTCTATT
970 980 990 1000 1010 1020

Fig.10c

T T T L A D G V P S R F S G S G S G T Q
ATACAACAACCTTAGCAGATGGTGTGCCATCAAGGTTTCAGTGGCAGTGGATCAGGAACAC
1030 1040 1050 1060 1070 1080

Y S L K I N S L Q P E D F G S Y Y C Q H
AATATTCTCTCAAGATCAACAGCCTGCAGCCTGAAGATTTTGGGAGTTATTACTGTCAAC
1090 1100 1110 1120 1130 1140

F W S T P R T F G G G T K L E I K R T V
ATTTTGGGAGTACTCTCTGGACGTTGGTGGAGGCCACCAAGCTCGAGATCAAACGGACTG
1150 1160 1170 1180 1190 1200

A A P S V F I F P P S D E Q L K S G T A
TGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGT
1210 1220 1230 1240 1250 1260

S V V C L L N N F Y P R E A K V Q W K V
CCTCTGTTGTGTGGCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGGAAGG
1270 1280 1290 1300 1310 1320

D N A L Q S G N S Q E S V T E Q D S K D
TGGATAAGGCCCTCCAATGGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGG
1330 1340 1350 1360 1370 1380

S T Y S L S S T L T L S K A D Y E K H K
ACAGCACTACAGCCTCAGCAGCA.CCCTGACGCTGAGCAAAGCAGACTACGAGAAACACA
1390 1400 1410 1420 1430 1440

V Y A C E V T H Q G L S S P V T K S F N
AAGTCTAAGCCTGGGAAGTCAACCATCAGGGCCTGAGCTGGCCCGTCACAAAGAGCTTCA
1450 1460 1470 1480 1490 1500

R G E S * * (SEQ ID NO. 188)
ACCGGGAGAGTCATAGTAAGAATTC (SEQ ID NO. 189)
1510 1520

Fig.10 d

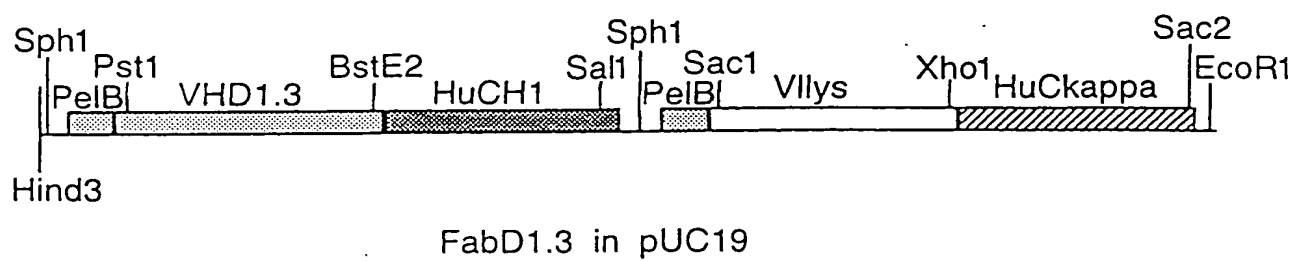


Fig.11.

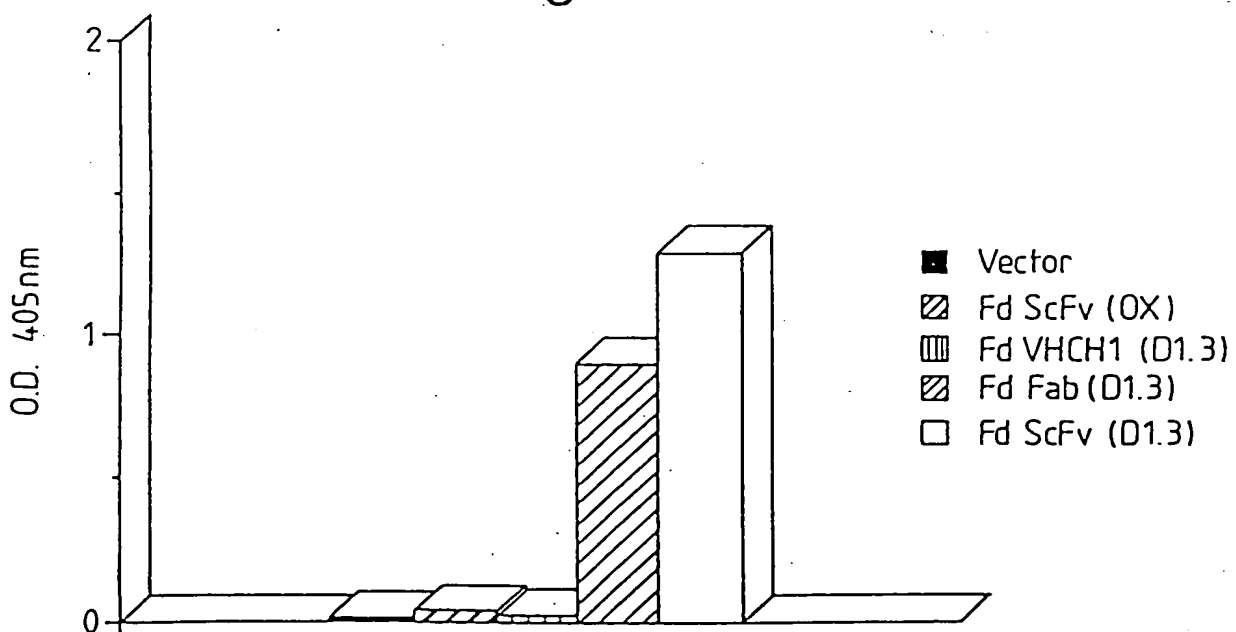


Fig.12a.

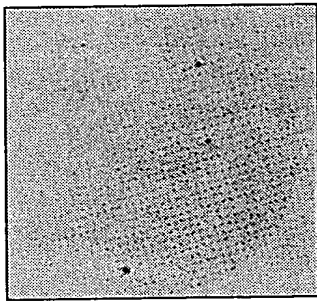


Fig.12b.

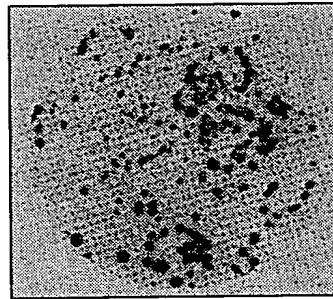


Fig.13.

Q V Q L Q E S G G G L V Q P G G
 CAG GTG CAG CTG CAG GAG TCA GGA GGA GGC TTG GTA CAG CCT GGG GGT
 PstI
 S L R L S C A T S G F T F S N Y
 TCT CTG AGA CTC TCC TGT GCA ACT TCT GGG TTC ACC TTC AGT AAT TAC
 Y M G W V R Q P P G K A L E W L
 TAC ATG GGC TGG GTC CGC CAG CCT CCA GGA AAG GCA CTT GAG TGG TTG
 G S V R N K V N G Y T T E Y S A
 GGT TCT GTT AGA AAC AAA GTT AAT GGT TAC ACA ACA GAG TAC AGT GCA
 S V K G R F T I S R D N F Q S I
 TCT GTG AAG GGG CGG TTC ACC ATC TCC AGA GAT AAT TTC CAA AGC ATC
 L Y L Q I N T L R T E D S A T Y
 CTC TAT CTT CAA ATA AAC ACC CTG AGA ACT GAG GAC AGT GCC ACT TAT
 Y C A R G Y D Y G A W F A Y W G
 TAC TGT GCA AGA GGC TAT GAT TAC GGG GCC TGG TTT GCT TAC TGG GGC
 Q G T L V T v s s g g g g s g g g g s
 CAA GGG ACC CTG GTC ACC gtc tcc tca ggtggaggcggttcaggcggaggtggctct
 BstEII
 g g g g s d i E L T Q T P L S L P V
 ggcggtggcggtatcgac atc GAG CTC ACC CAA ACT CCA CTC TCC CTG CCT GTC
 SacI
 S L G D Q A S I S C R S S Q S I
 AGT CTT GGA GAT CAA GCC TCC ATC TCT TGC AGA TCT AGT CAG AGC ATT
 V H S N G N T Y L E W Y L Q K P
 GTA CAT AGT AAT GGA AAC ACC TAT TTA GAA TGG TAC CTG CAG AAA CCA
 PstI
 G Q S P K L L I Y K V S N R F S
 GGC CAG TCT CCA AAG CTC CTG ATC TAC AAA GTT TCC AAC CGA TTT TCT
 G V P D R F S G S G S G T D F T
 GGG GTC CCA GAC AGG TTC AGT GGC AGT GGA TCG GGG ACA GAT TTC ACA
 L K I S R V E A E D L G V Y Y C
 CTC AAG ATC AGC AGA GTG GAG GCT GAG GAT CTG GGA GTT TAT TAC TGC
 F Q G S H V P Y T F G G G T K L
 TTT CAA GGT TCA CAT GTT CCG TAC ACG TTC GGA GGG GGG ACC AAG CTC
 E I K R
GAG ATC AAA CGG (SEQ ID NO. 190)
 XhoI (SEQ ID NO. 191)

Fig.14.

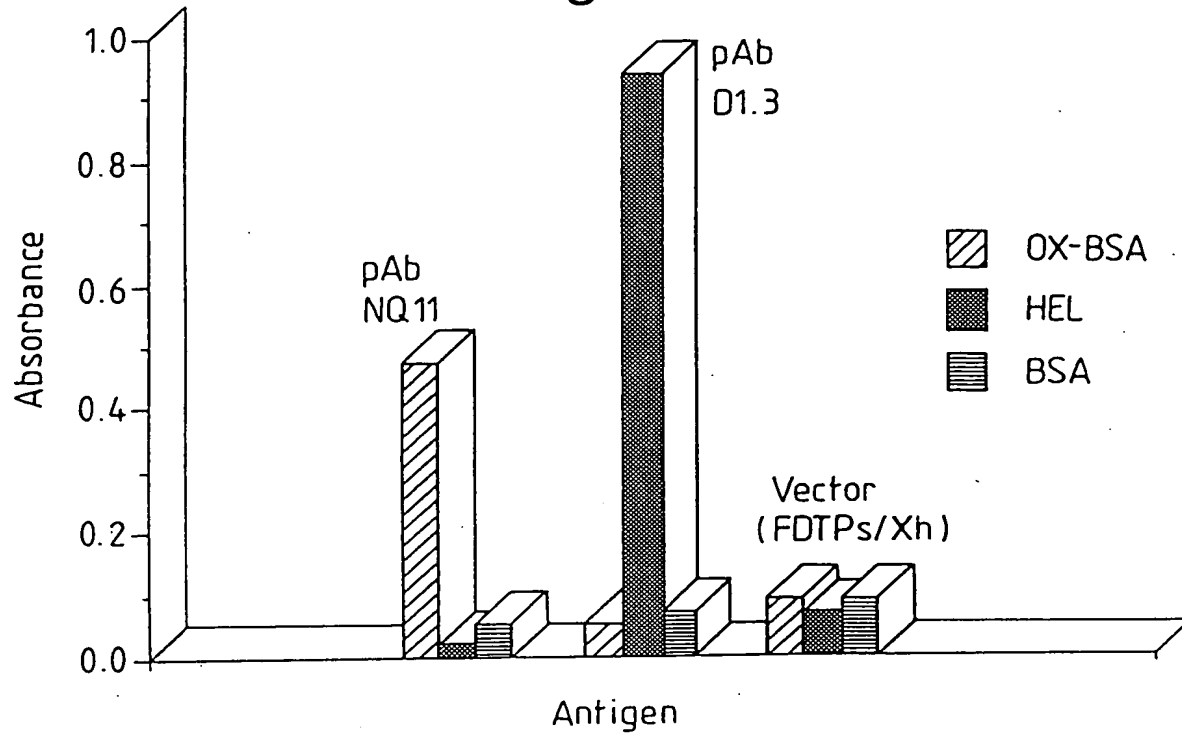


Fig.15.

5' END

TCT CAC AGT GCA CAA ACT GTT GAA CGG ACA CCA GAA ATG CCT GTT CTG (SEQ ID NO:192)
 (SEQ ID NO:193)
 ApaL1

3' END

K A A L G L K (SEQ ID NO:194)
 AAA GCC GCT CTG GGG CTG AAA GCG GCC GCA GAA ACT GTT GAA AGT etc. (SEQ ID NO:195)
 Not I

Fig.16a

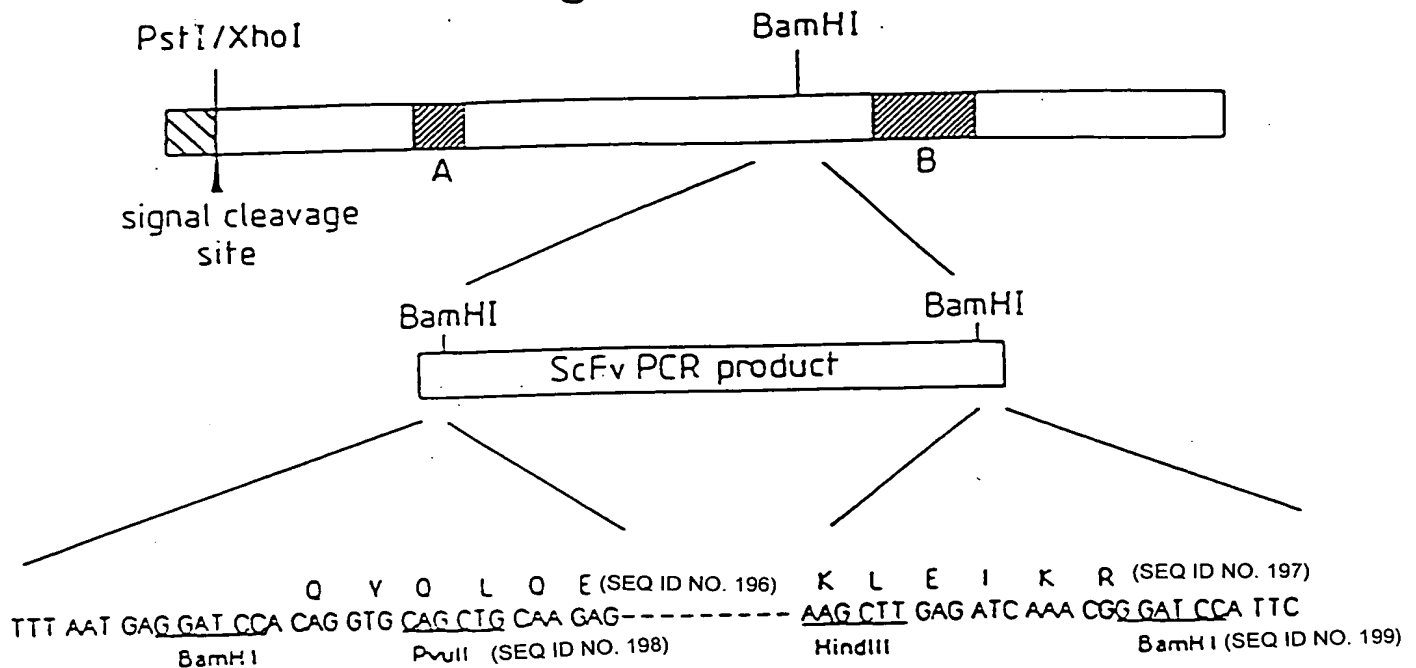
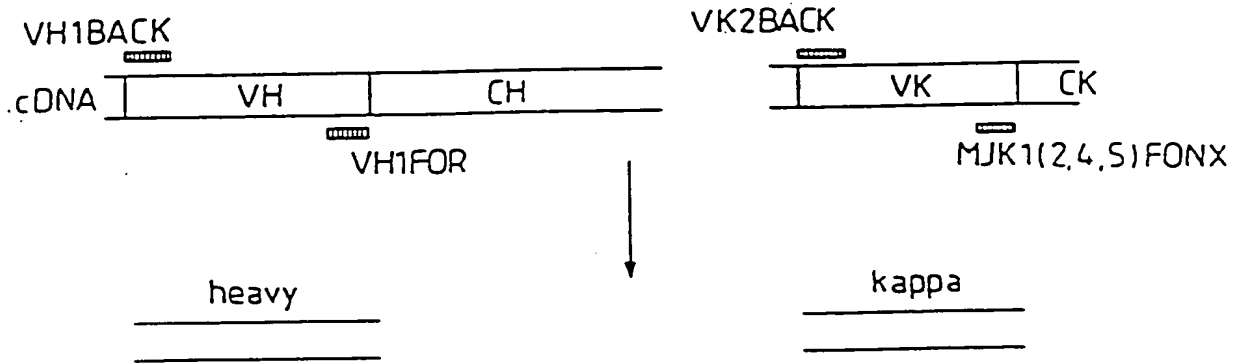


Fig.16b

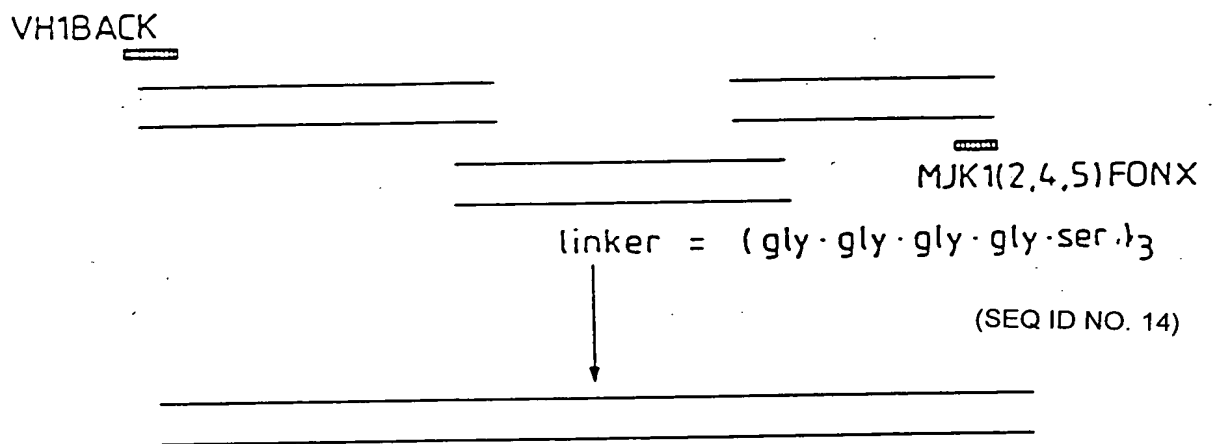
A	(1834)	5'	GAG GGT GGT GGC TCT	(SEQ ID NO. 200)
		-	- -C - -	(SEQ ID NO. 201)
		-	- -C - -	(SEQ ID NO. 202)
		-	- -C - -	ACT 3' (1839) (SEQ ID NO. 203)
B	(2284)	5'	GGC GGC GGC TCT	(SEQ ID NO. 204)
		-	GGT GGT GGT -	(SEQ ID NO. 205)
		-	- GGC GGC -	(SEQ ID NO. 206)
		GAG	- - GGC -	(SEQ ID NO. 207)
		-	- - GGT -	(SEQ ID NO. 208)
		-	- - GGC -	(SEQ ID NO. 209)
		-	- - GGT -	(SEQ ID NO. 210)
		-	- - GGC -	3' (2379) (SEQ ID NO. 211)
Reverse complement of mutagenic oligo				
		5'	GAG GGT GGC GGA TCC	(SEQ ID NO. 212)
			T	
			GAG GGT GGC GG 3'	(SEQ ID NO. 213)

Fig.17.

1) PRIMARY PCR



2) ASSEMBLY PCR



3) ADDING RESTRICTION SITES

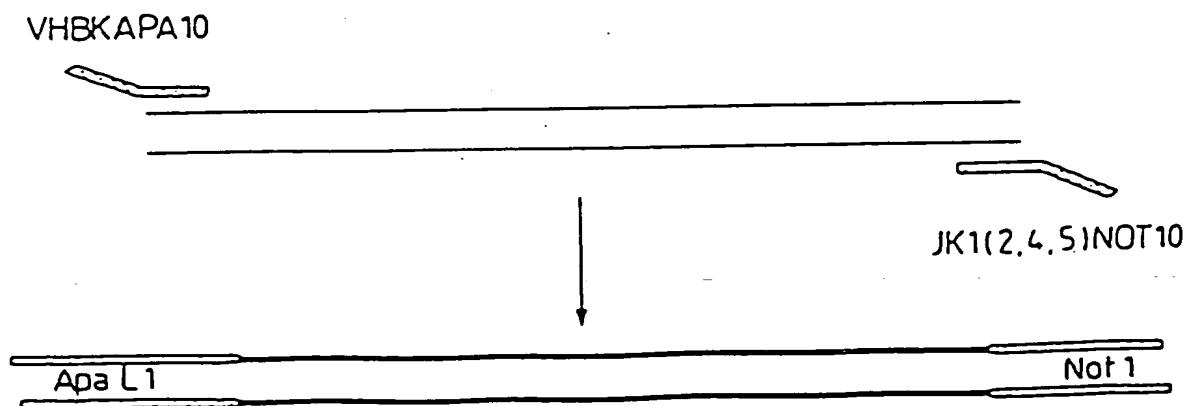


Fig.18.

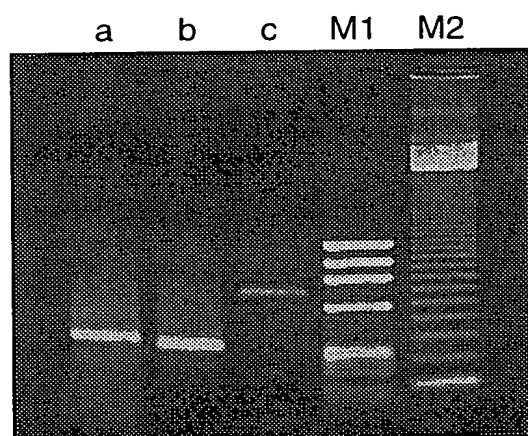


Fig.19.

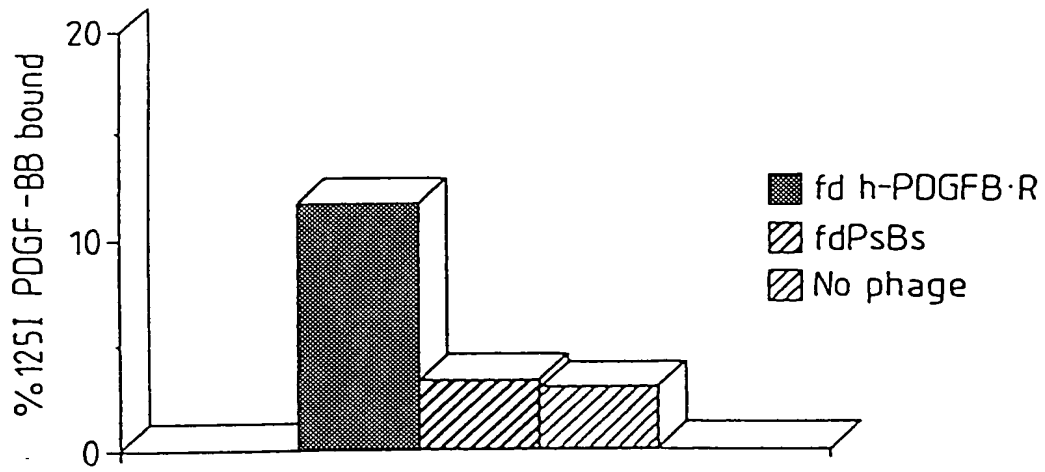


Fig.20.

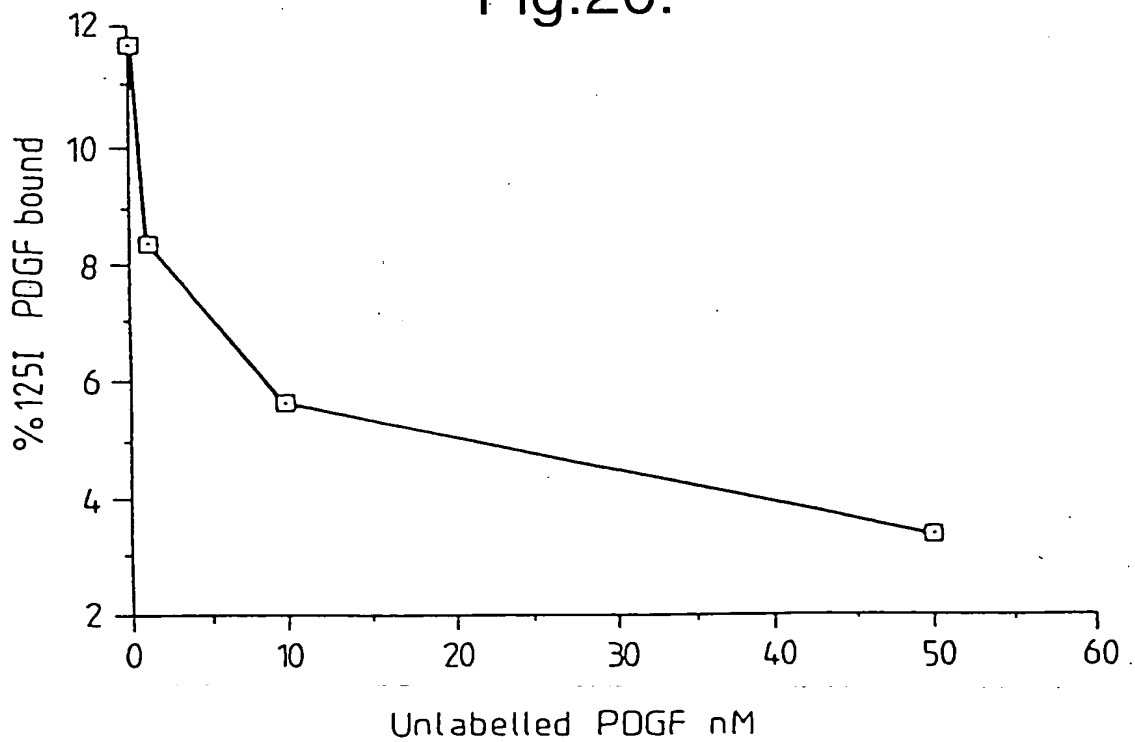


Fig.21.

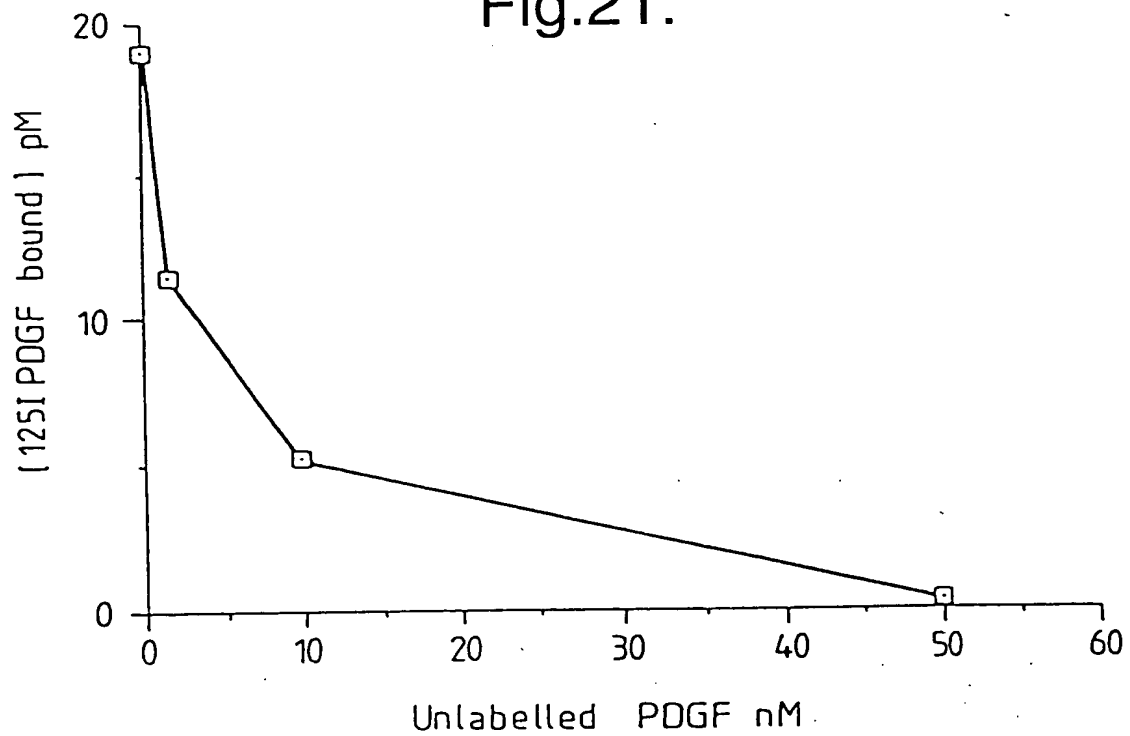


Fig.22.

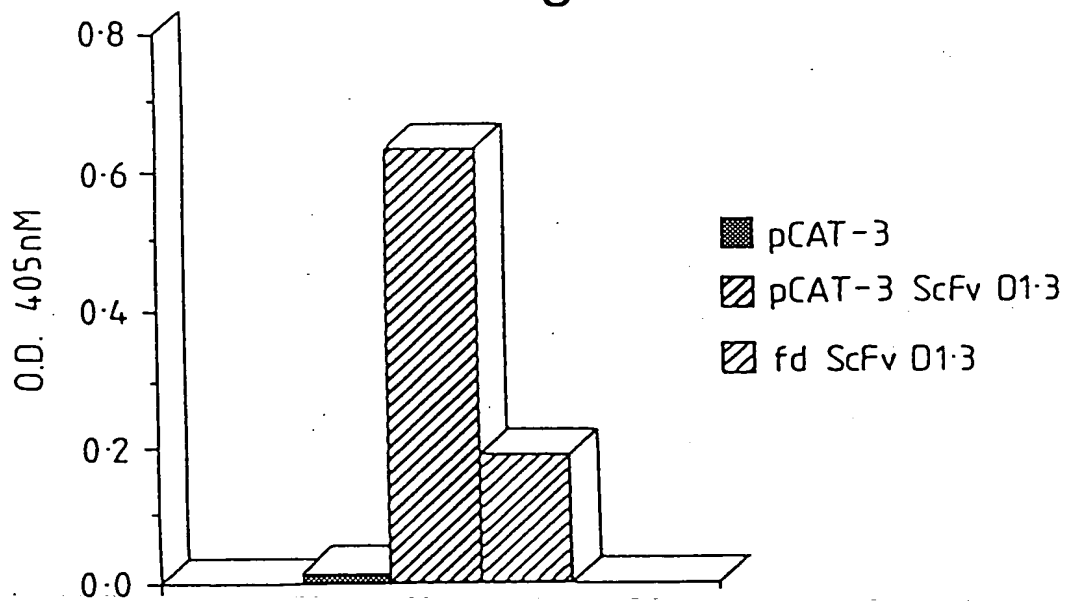


Fig.23a

d
M

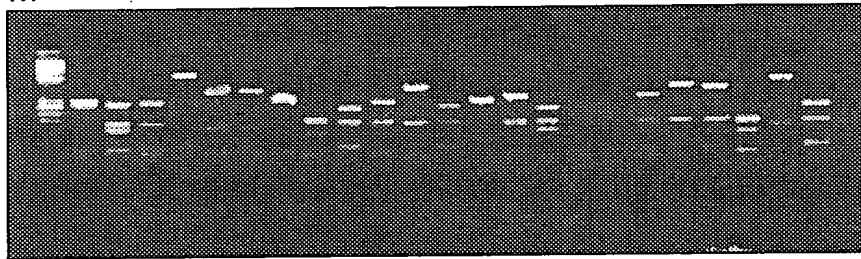


Fig.23b

M

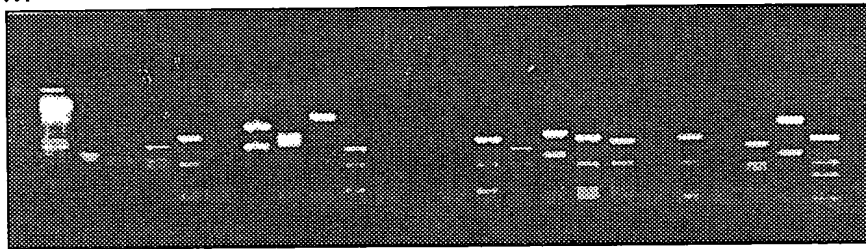


Fig.24a

VH sequences

from combinatorial library:

	CDR1	CDR2	CDR3		
A	QVQLQSGSGLASGVTGHSCKASGTTT	YINPSEGYNTHNQKFKD	KATLTADKSSSTAYHQLSSLTSEDSAVTYCAH	HCQGTITVTS9 x4	(SEQ ID NO. 214)
B	QVQLQSGSGLASGVTGHSCKASGTTT	YINPSEGYNTHNQKFKD	KATLTADKSSSTAYHQLSSLTSEDSAVTYCAH	HCQGTITVTS9 x9	(SEQ ID NO. 215)
C	QVQLQSGSGLASGVTGHSCKASGTTT	YINPSEGYNTHNQKFKD	KATLTADKSSSTAYHQLSSLTSEDSAVTYCAH	HCQGTITVTS9 x3	(SEQ ID NO. 216)
D	QVQLQSGSGLASGVTGHSCKASGTTT	YINPSEGYNTHNQKFKD	KATLTADKSSSTAYHQLSSLTSEDSAVTYCAH	HCQGTITVTS9 x3	(SEQ ID NO. 217)
E	QVQLQSGSGLASGVTGHSCKASGTTT	YINPSEGYNTHNQKFKD	KATLTADKSSSTAYHQLSSLTSEDSAVTYCAH	HCQGTITVTS9 x3	(SEQ ID NO. 218)
F	QVQLQSGSGLASGVTGHSCKASGTTT	YINPSEGYNTHNQKFKD	KATLTADKSSSTAYHQLSSLTSEDSAVTYCAH	HCQGTITVTS9 x3	(SEQ ID NO. 219)
G	QVQLQSGSGLASGVTGHSCKASGTTT	YINPSEGYNTHNQKFKD	KATLTADKSSSTAYHQLSSLTSEDSAVTYCAH	HCQGTITVTS9 x3	(SEQ ID NO. 220)
H	QVQLQSGSGLASGVTGHSCKASGTTT	YINPSEGYNTHNQKFKD	KATLTADKSSSTAYHQLSSLTSEDSAVTYCAH	HCQGTITVTS9 x3	(SEQ ID NO. 221)

from hierarchical library VH-rep x Vd-d:

	CDR1	CDR2	CDR3		
I	QVQLQSGSGLASGVTGHSCKASGTTT	YINPSEGYNTHNQKFKD	KATLTADKSSSTAYHQLSSLTSEDSAVTYCAH	HCQGTITVTS9	(SEQ ID NO. 222)
J	QVQLQSGSGLASGVTGHSCKASGTTT	YINPSEGYNTHNQKFKD	KATLTADKSSSTAYHQLSSLTSEDSAVTYCAH	HCQGTITVTS9	(SEQ ID NO. 223)
K	QVQLQSGSGLASGVTGHSCKASGTTT	YINPSEGYNTHNQKFKD	KATLTADKSSSTAYHQLSSLTSEDSAVTYCAH	HCQGTITVTS9 x3	(SEQ ID NO. 224)
L	QVQLQSGSGLASGVTGHSCKASGTTT	YINPSEGYNTHNQKFKD	KATLTADKSSSTAYHQLSSLTSEDSAVTYCAH	HCQGTITVTS9 x3	(SEQ ID NO. 225)
M	QVQLQSGSGLASGVTGHSCKASGTTT	YINPSEGYNTHNQKFKD	KATLTADKSSSTAYHQLSSLTSEDSAVTYCAH	HCQGTITVTS9	(SEQ ID NO. 226)
N	QVQLQSGSGLASGVTGHSCKASGTTT	YINPSEGYNTHNQKFKD	KATLTADKSSSTAYHQLSSLTSEDSAVTYCAH	HCQGTITVTS9	(SEQ ID NO. 227)
O	QVQLQSGSGLASGVTGHSCKASGTTT	YINPSEGYNTHNQKFKD	KATLTADKSSSTAYHQLSSLTSEDSAVTYCAH	HCQGTITVTS9	(SEQ ID NO. 228)
P	QVQLQSGSGLASGVTGHSCKASGTTT	YINPSEGYNTHNQKFKD	KATLTADKSSSTAYHQLSSLTSEDSAVTYCAH	HCQGTITVTS9	(SEQ ID NO. 229)
Q	QVQLQSGSGLASGVTGHSCKASGTTT	YINPSEGYNTHNQKFKD	KATLTADKSSSTAYHQLSSLTSEDSAVTYCAH	HCQGTITVTS9	(SEQ ID NO. 230)
R	QVQLQSGSGLASGVTGHSCKASGTTT	YINPSEGYNTHNQKFKD	KATLTADKSSSTAYHQLSSLTSEDSAVTYCAH	HCQGTITVTS9	(SEQ ID NO. 231)
S	QVQLQSGSGLASGVTGHSCKASGTTT	YINPSEGYNTHNQKFKD	KATLTADKSSSTAYHQLSSLTSEDSAVTYCAH	HCQGTITVTS9	(SEQ ID NO. 232)
T	QVQLQSGSGLASGVTGHSCKASGTTT	YINPSEGYNTHNQKFKD	KATLTADKSSSTAYHQLSSLTSEDSAVTYCAH	HCQGTITVTS9 x3	(SEQ ID NO. 233)
U	QVQLQSGSGLASGVTGHSCKASGTTT	YINPSEGYNTHNQKFKD	KATLTADKSSSTAYHQLSSLTSEDSAVTYCAH	HCQGTITVTS9 x6	(SEQ ID NO. 234)
V	QVQLQSGSGLASGVTGHSCKASGTTT	YINPSEGYNTHNQKFKD	KATLTADKSSSTAYHQLSSLTSEDSAVTYCAH	HCQGTITVTS9	(SEQ ID NO. 235)

Fig.24b

Vx sequences

from combinatorial library:

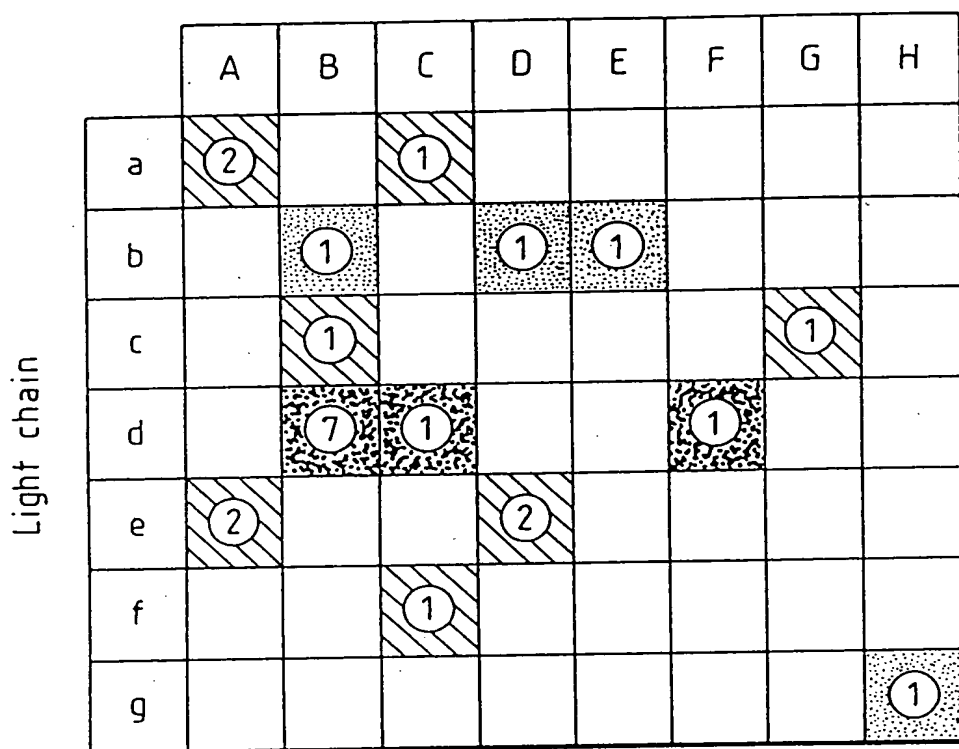
	CDRI	CDR2	CDR3		
a	DIELTQSPSSLSASLCGERVSLTC	WLOQKPDGSIKRLIY	AASTLES	OVVPARFSGRSGDYSLTISLSLESEDFADYYC	LOVASYPPT
b	DIELTQSPA IHSASPGCKVNTTC	MYQQKSGASPKRMIIY	BTSHLAS	OVVPARFSGSGCTGYSLTISSEVEDAATYYC	QQYSGYPLT
c	DIELTQSPPTTHAASPGCKITITC	MYQQKPGFSPKLLIY	RTSHLAS	OVVPARFSGSGCTSYSLTIGTHEAEDVAATYYC	QQGSSIPLT
d	DIELTQSPPTTHAASPGCKITITC	MYQQKPGFSPKLLIS	RTSHLAS	OVVPARFSGSGCTSYSLTIGTHEAEDVAATYYC	QQGSTIPPT
e	DIELTQSPA IHSASPGCKVNTTC	MYQQKPGTSPKLMIIY	STSHLAS	OVVPARFSGSGCTSYSLTISSEVEDAATYYC	QQRSSYPPT
f	DIELTQSPA IHSASPGCKVNTTC	MYQQKSGTSPKRMIIY	DTSKLAS	OVVPARFSGSGCTSYSLTISSEVEDAATYYC	QQFSNIPLT
g	DIELTQSPA IHSASPGCKVNTTC	MYQQKPGASPKRMIIY	DTSKLAS	OVVPARFSGSGCTSYSLTISSEVEDAATYYC	IQRNISYPPT

from hierarchical library VH-B x Vx-rep:

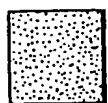
h	DIELTQSPA IHSASPGCKVNTTC	SASSSVSTTHI	DTSKLAG	OVVPARFSGSGCTSYSLTISSEVEDAATYYC	QQMSNPILT	FGAGTKLEIKRA	x4	IV/VI	Vxox1	(SEQ ID NO. 243)
i	DIELTQSPA IHSASPGCKVNTTC	SASSSVSTTHI	STSHLAG	OVVPARFSGSGCTSYSLTISSEVEDAATYYC	QQYHSYPLT	FGAGTKLEIKRA	x3	V	ox-1like?	(SEQ ID NO. 244)
j	DIELTQSPPTTHAASPGCKITITC	SASSSVSTTHI	RTSHLAG	OVVPARFSGSGCTSYSLTIGTHEAEDVAATYYC	QQGSSIPLT	FGAGTKLEIKRA	x3	V	ox-1like	(SEQ ID NO. 245)
k	DIELTQSPPTTHAASPGCKITITC	SASSSVSTTHI	RTSHLAG	OVVPARFSGSGCTSYSLTIGTHEAEDVAATYYC	QQGSSIPLT	FGAGTKLEIKRA	x3	V	ox-1like	(SEQ ID NO. 246)
l	DIELTQSPPTTHAASPGCKITITC	SASSSVSTTHI	RTSHLAG	OVVPARFSGSGCTSYSLTIGTHEAEDVAATYYC	QQGSSIPLT	FGAGTKLEIKRA	x3	V	ox-1like	(SEQ ID NO. 247)
m	DIELTQSPPTTHAASPGCKITITC	SASSSVSTTHI	RTSHLAG	OVVPARFSGSGCTSYSLTIGTHEAEDVAATYYC	QQGSSIPLT	FGAGTKLEIKRA	x3	V	ox-1like	(SEQ ID NO. 248)
n	DIELTQSPPTTHAASPGCKITITC	SASSSVSTTHI	RTSHLAG	OVVPARFSGSGCTSYSLTIGTHEAEDVAATYYC	QQGSSIPLT	FGAGTKLEIKRA	x3	V	ox-1like	(SEQ ID NO. 249)
o	DIELTQSPA IHSASPGCKVNTTC	SASSSVSTTHI	RTSHLAG	OVVPARFSGSGCTSYSLTIGTHEAEDVAATYYC	QQGSSIPLT	FGAGTKLEIKRA	x3	V	ox-1like	(SEQ ID NO. 250)
p	DIELTQSPA IHSASPGCKVNTTC	SASSSVSTTHI	RTSHLAG	OVVPARFSGSGCTSYSLTIGTHEAEDVAATYYC	QQGSSIPLT	FGAGTKLEIKRA	x3	V	ox-1like	(SEQ ID NO. 251)
q	DIELTQSPA IHSASPGCKVNTTC	SASSSVSTTHI	RTSHLAG	OVVPARFSGSGCTSYSLTIGTHEAEDVAATYYC	QQGSSIPLT	FGAGTKLEIKRA	x3	V	ox-1like	(SEQ ID NO. 252)
r	DIELTQSPA IHSASPGCKVNTTC	SASSSVSTTHI	RTSHLAG	OVVPARFSGSGCTSYSLTIGTHEAEDVAATYYC	QQGSSIPLT	FGAGTKLEIKRA	x3	V	ox-1like	(SEQ ID NO. 253)
s	DIELTQSPA IHSASPGCKVNTTC	SASSSVSTTHI	RTSHLAG	OVVPARFSGSGCTSYSLTIGTHEAEDVAATYYC	QQGSSIPLT	FGAGTKLEIKRA	x3	V	ox-1like	(SEQ ID NO. 254)
t	DIELTQSPA IHSASPGCKVNTTC	SASSSVSTTHI	RTSHLAG	OVVPARFSGSGCTSYSLTIGTHEAEDVAATYYC	QQGSSIPLT	FGAGTKLEIKRA	x3	V	ox-1like	(SEQ ID NO. 255)
u	DIELTQSPA IHSASPGCKVNTTC	SASSSVSTTHI	RTSHLAG	OVVPARFSGSGCTSYSLTIGTHEAEDVAATYYC	QQGSSIPLT	FGAGTKLEIKRA	x3	V	ox-1like	(SEQ ID NO. 256)
v	DIELTQSPA IHSASPGCKVNTTC	SASSSVSTTHI	RTSHLAG	OVVPARFSGSGCTSYSLTIGTHEAEDVAATYYC	QQGSSIPLT	FGAGTKLEIKRA	x3	V	ox-1like	(SEQ ID NO. 257)
w	DIELTQSPA IHSASPGCKVNTTC	SASSSVSTTHI	RTSHLAG	OVVPARFSGSGCTSYSLTIGTHEAEDVAATYYC	QQGSSIPLT	FGAGTKLEIKRA	x3	V	ox-1like	(SEQ ID NO. 258)

Fig.25.

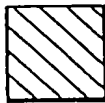
HEAVY CHAIN



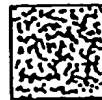
OD_{405nm} in ELISA



0.2-0.9



0.9-2.0



>2.0

Fig.26(a).

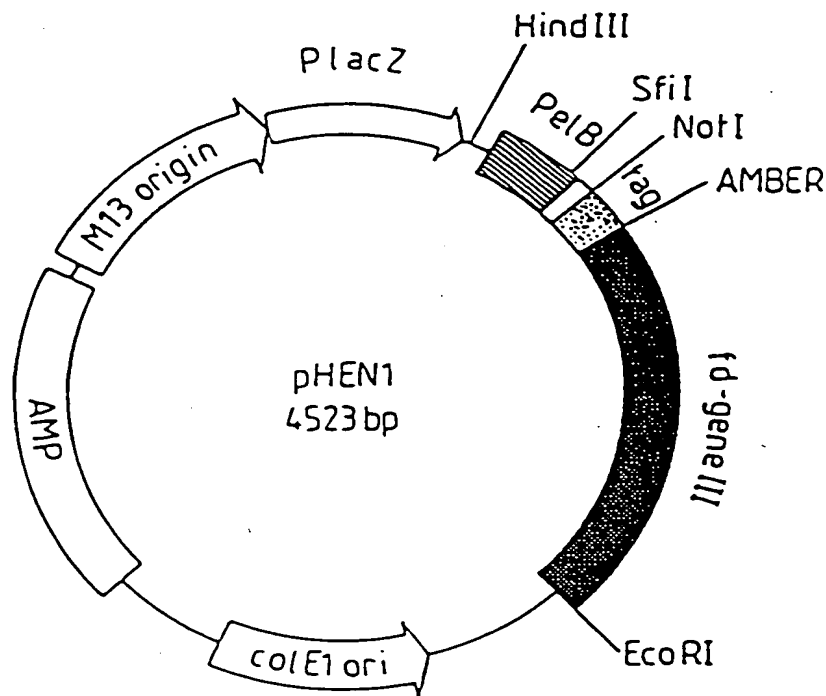


Fig.26(b).

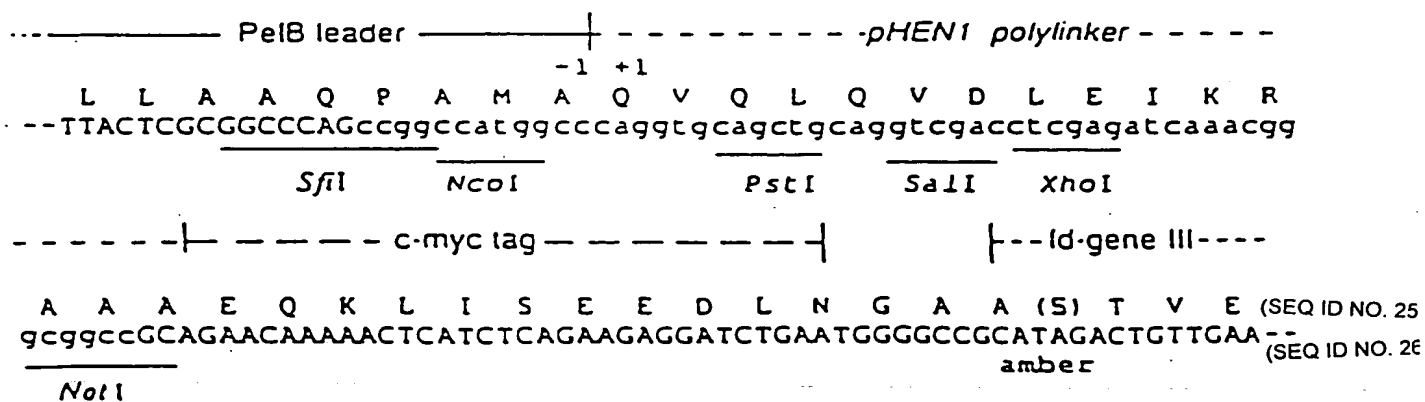


Fig.27.

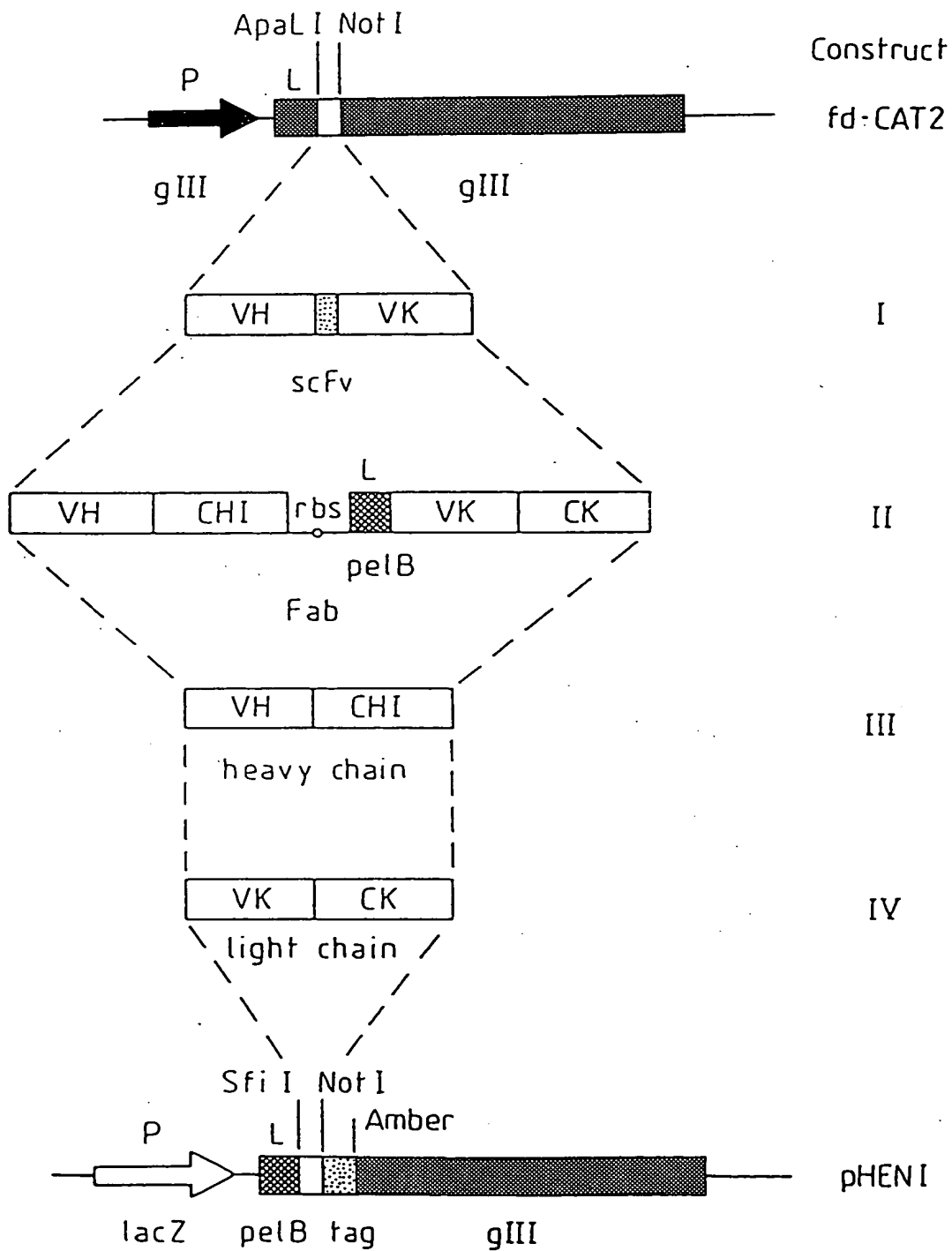


Fig.28.

Fab

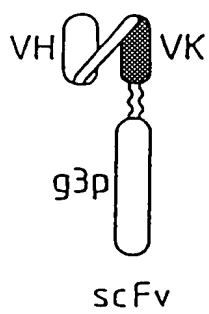
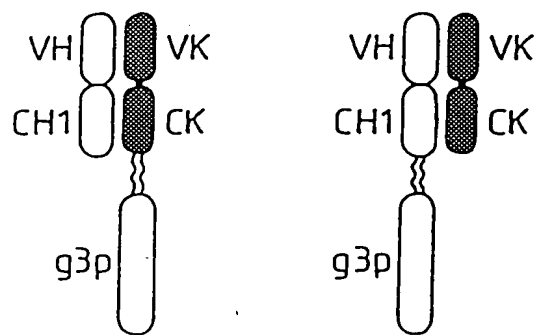


Fig.29.

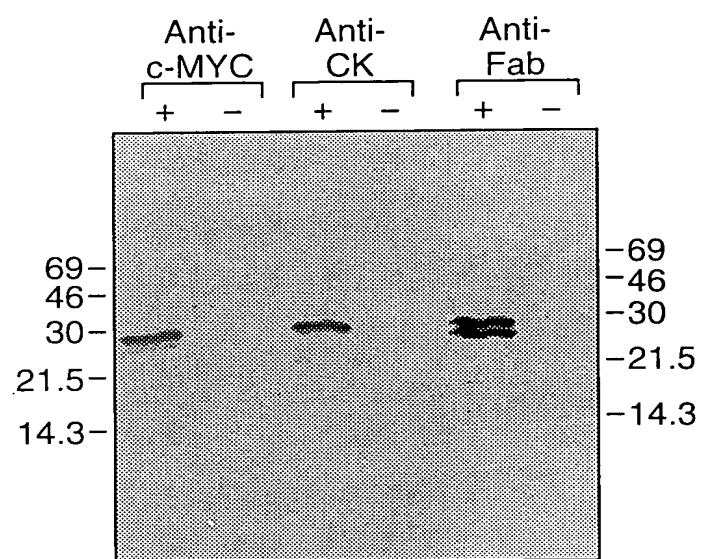


Fig.30.

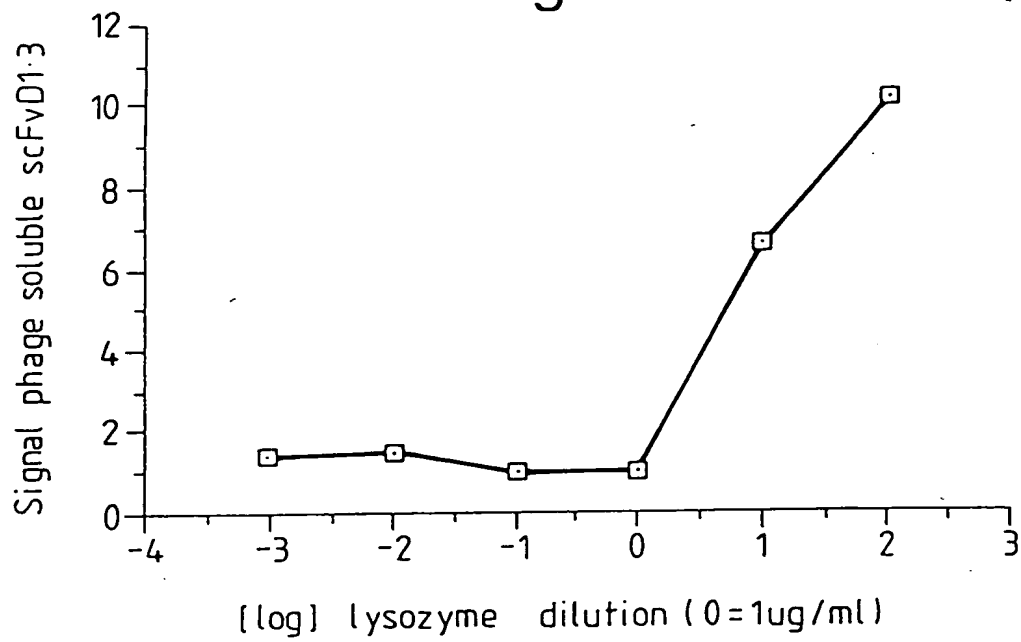


Fig.31.

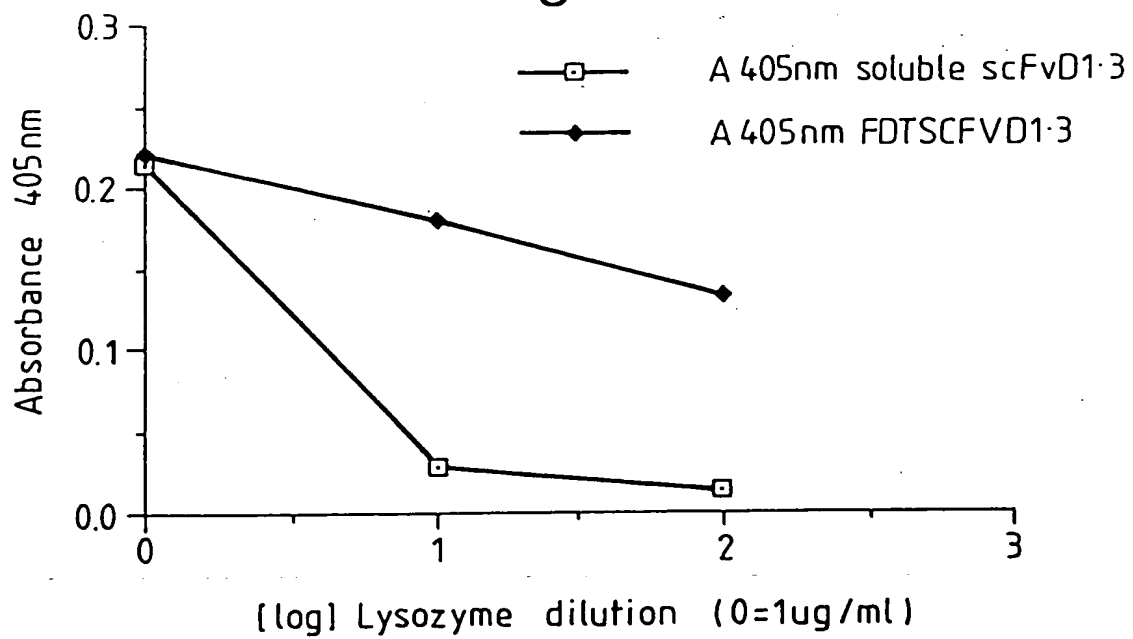


Fig.32.

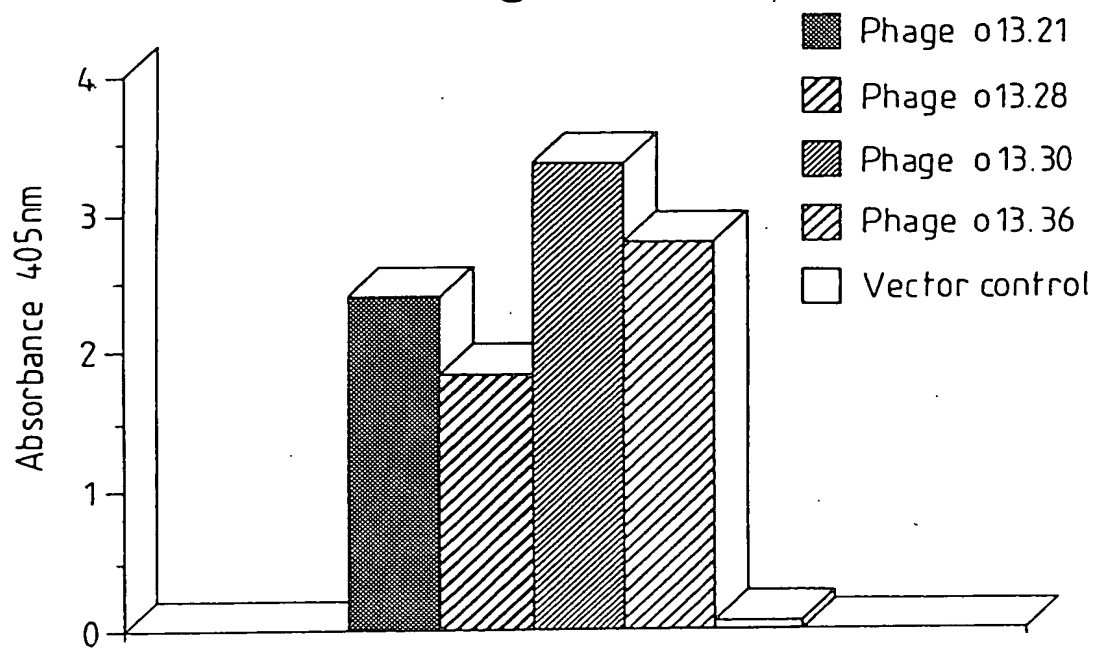


Fig.33.

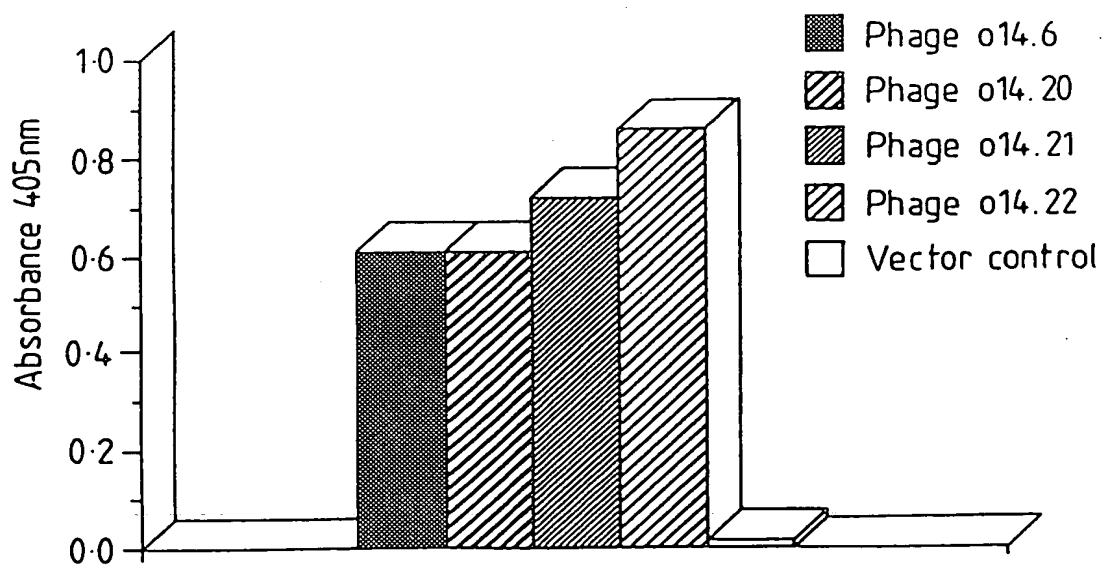


Fig.34.

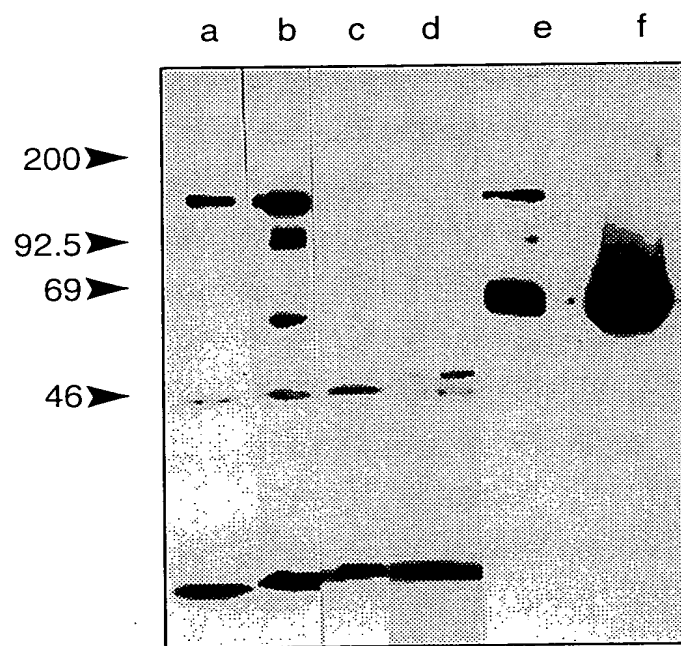


Fig.35A.

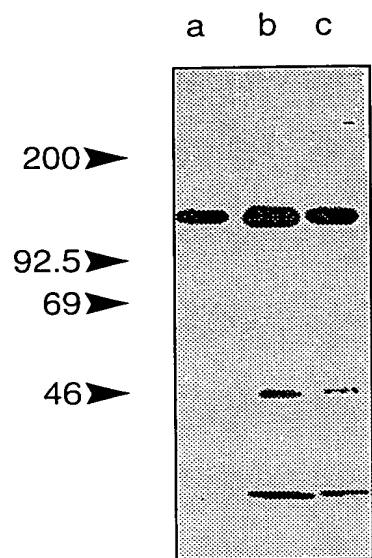


Fig.35B.

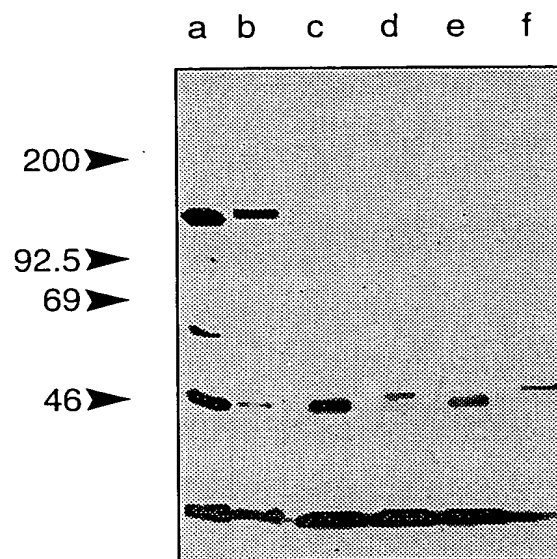


Fig.36.

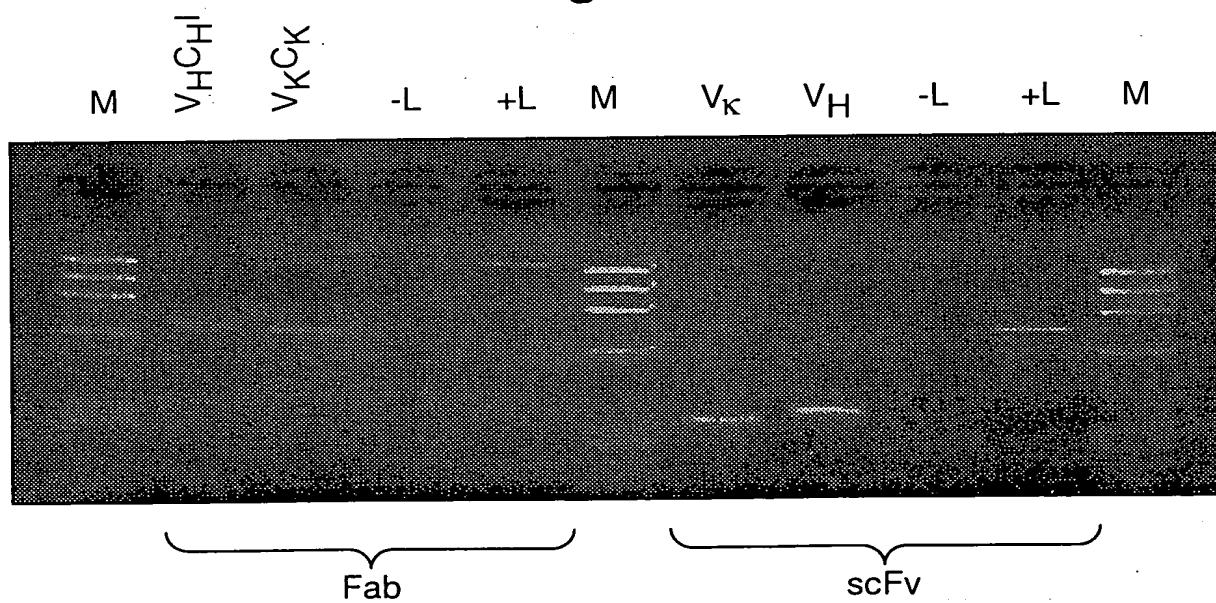


Fig.37.

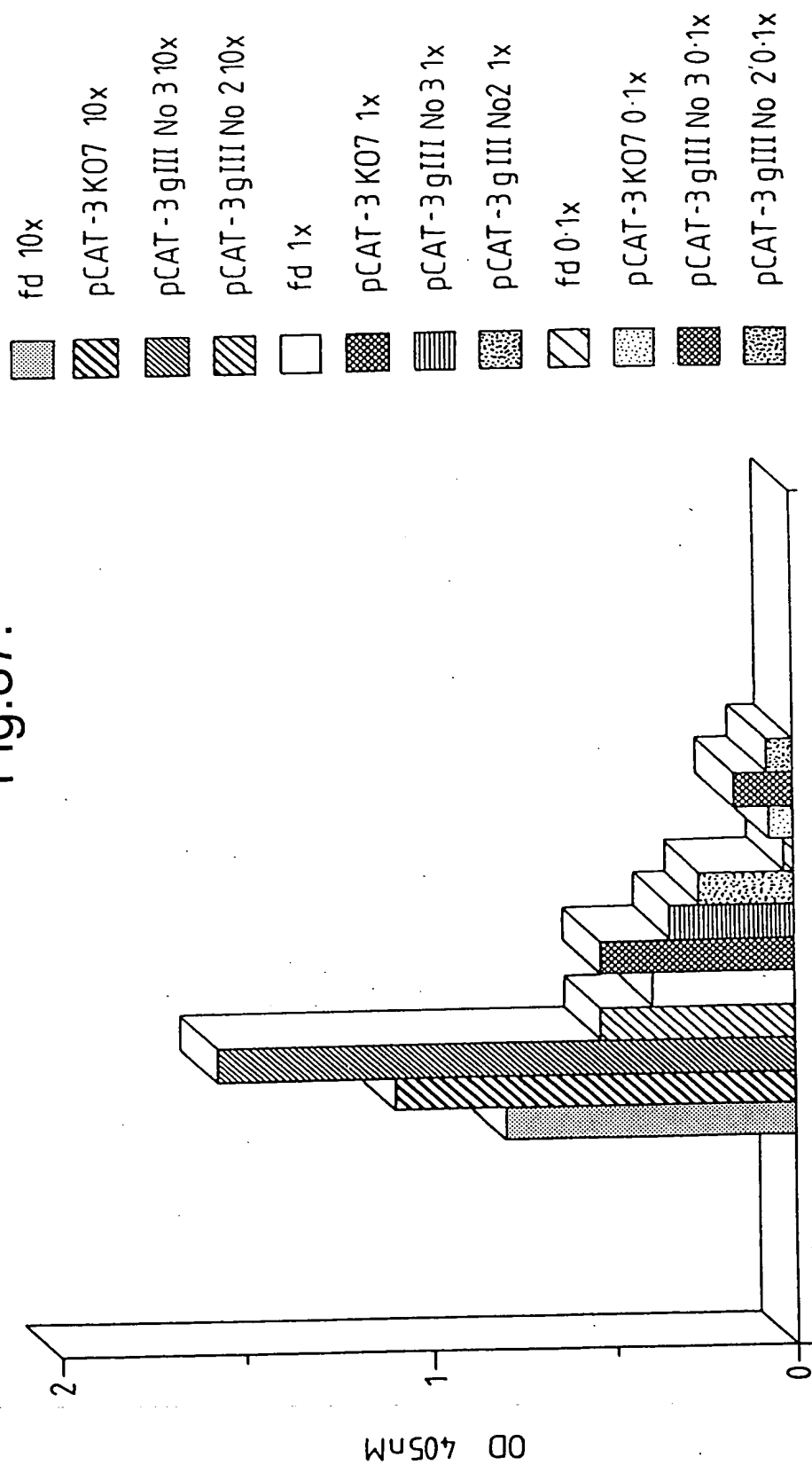


Fig.38A.

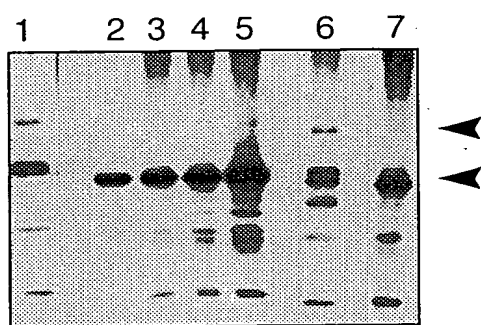


Fig.38B.

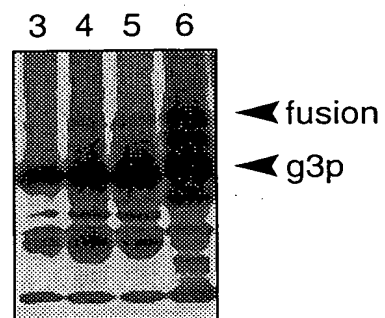


Fig.39.

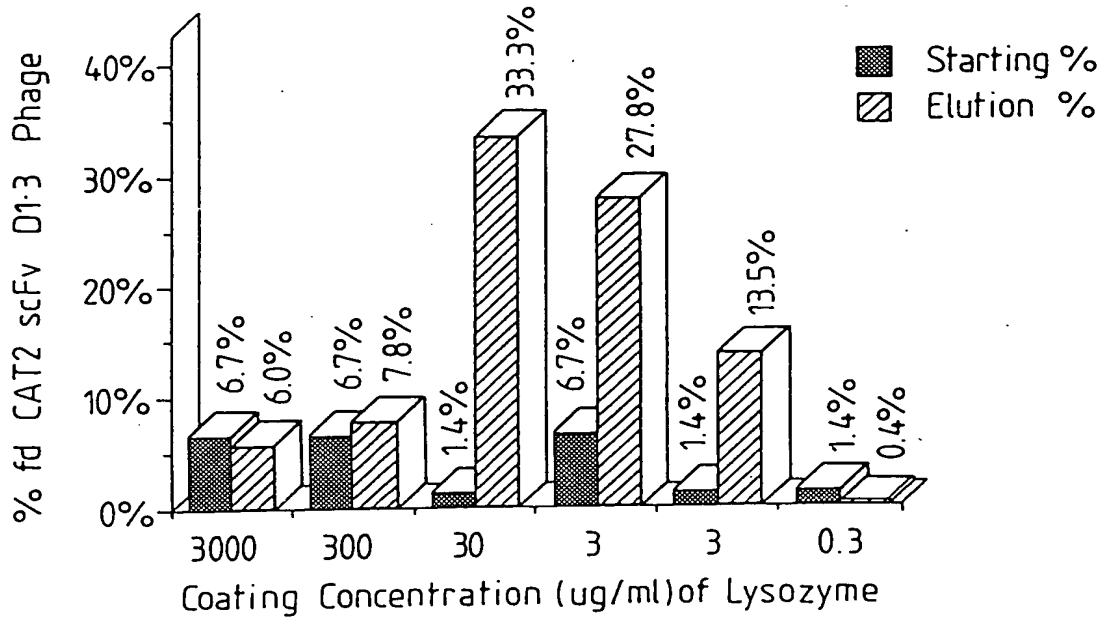


Fig.40.

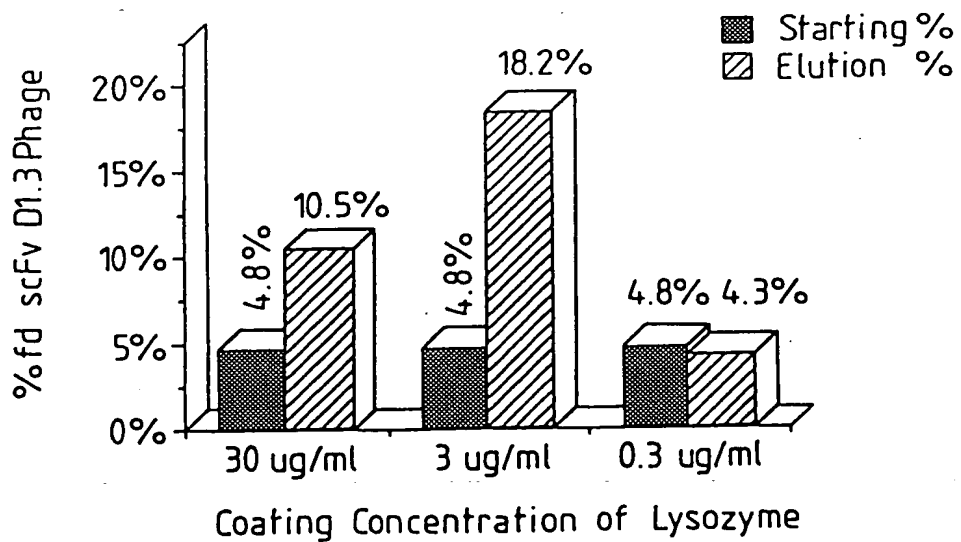


Fig.41.

1 2

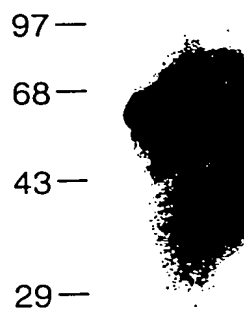


Fig.42.

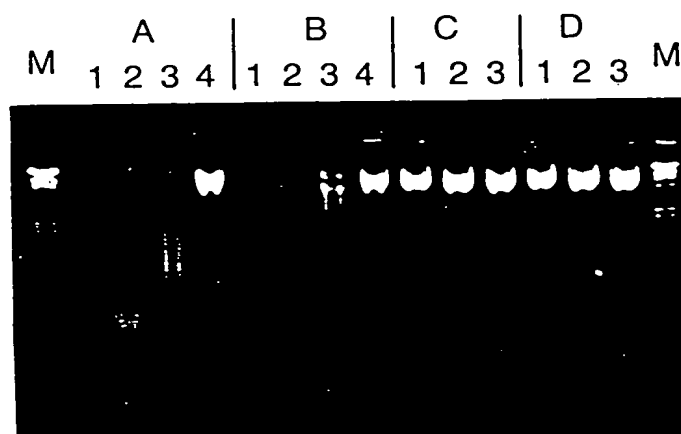
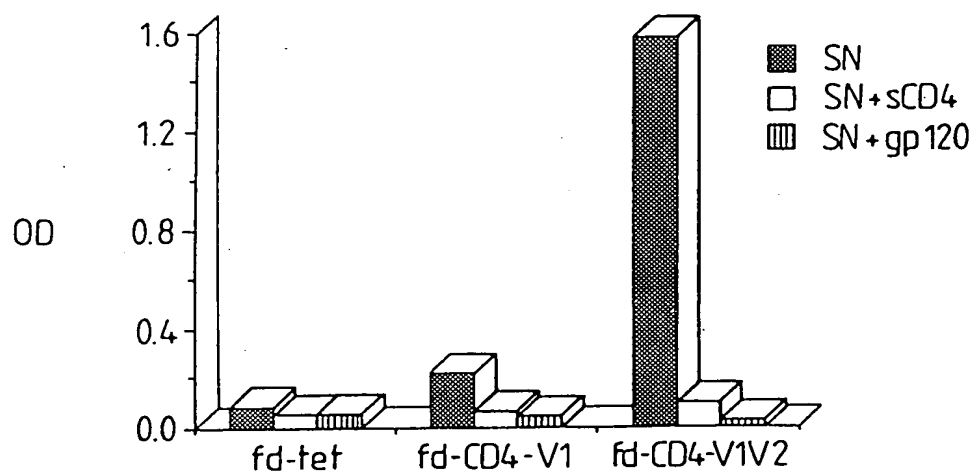


Fig.43.



[illegible]

Fig.44 b

640	650	660	670	680	690	700	C	G	710	720
GGAGACAAGGCTGCCCCCTCACCATCACAGGGGCACAGACTGAGGATGAGGCANTATATTCTGTGCTCTATGGTACAGCAACCAATTGGGTG										
CCTCTGTTCCGACGGAGTGGTAGTGTCCTCCCGTGTCTGACTCCTACTCCGTTATATAAGACACGAGATACCATGTGCTGGTAACCCAC										
GlyAspLysAlaAlaLeuThrIleThrGlyAlaGlnThrGluAspGluAlaIleTyrPheCysAlaLeuTrpTyrnberAsnHisTrpVal										
730	740	750	760	770						
TTCGGTGAGGAAACCAAACTGACTGTCTCGAGATCAAAACGGCGGCCGC										
AAGCCACCTCCTTGTTGACTGACAGGAGCTCTAGTTGCCCGCCGCGG										
PheGlyGlyGlyThrLysLeuThrValLeuGluIleLysArgAlaAla										

(SEQ ID NO. 261)

(SEQ ID NO. 262)

Fig.45.

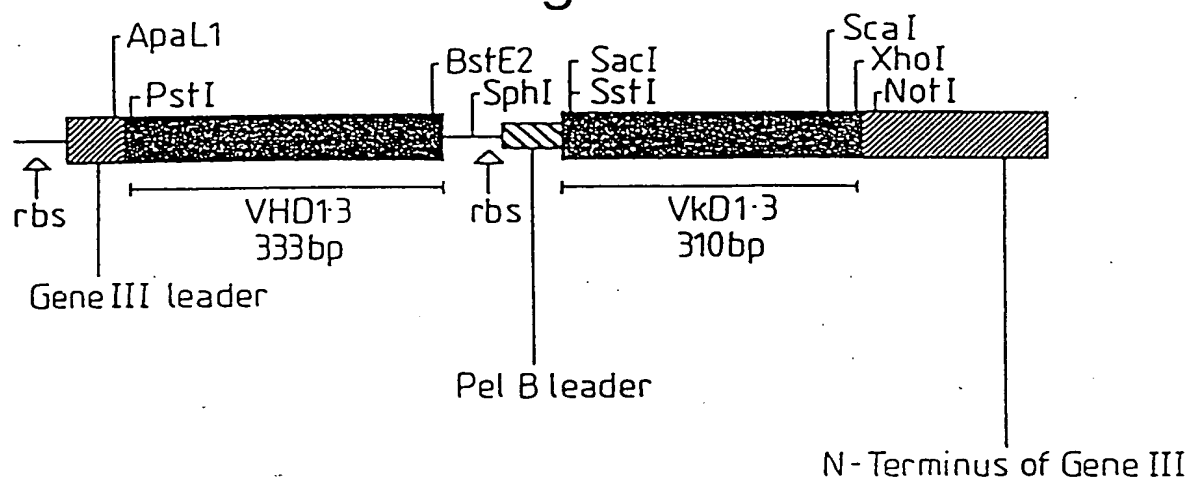


Fig.46.

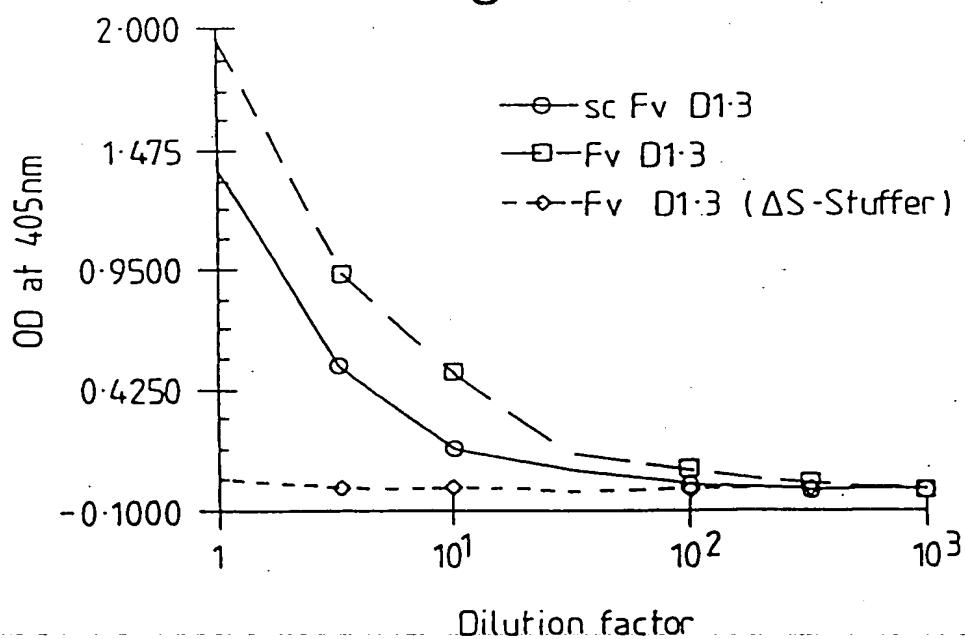


Fig.47.

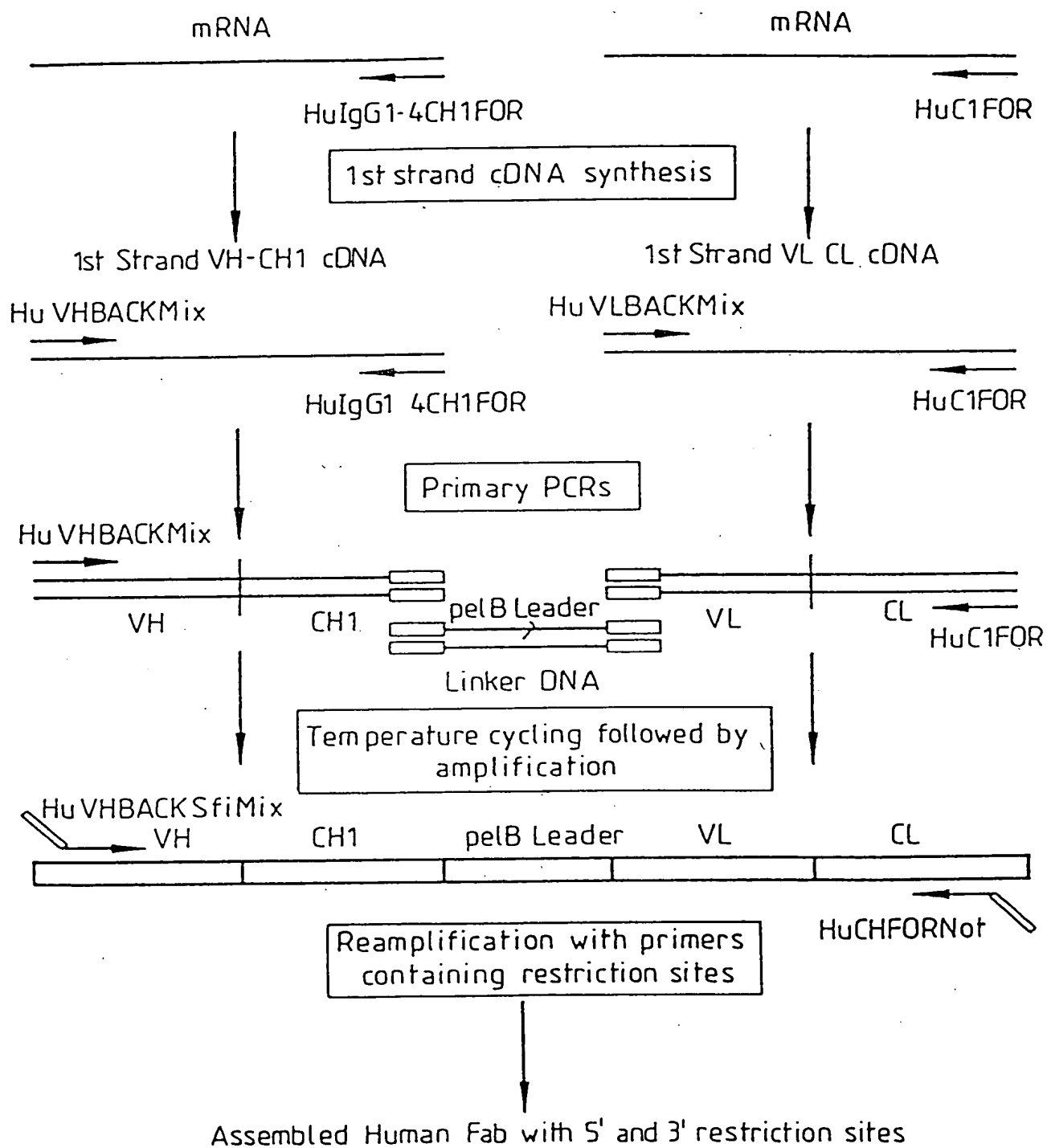


Fig. 48a

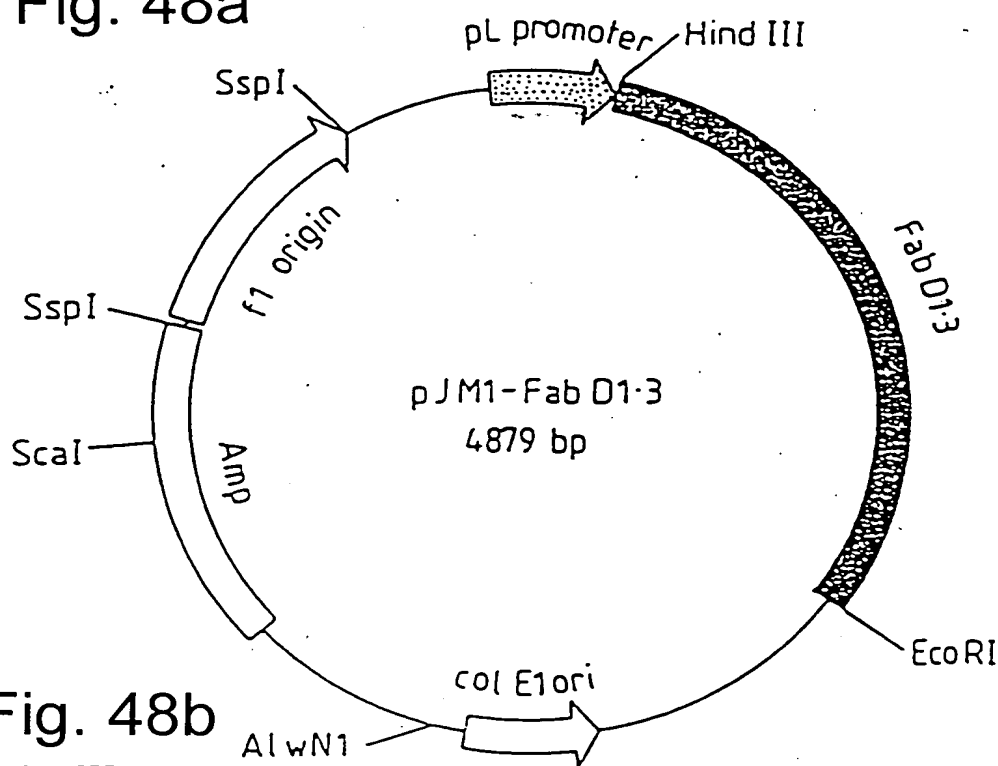


Fig. 48b

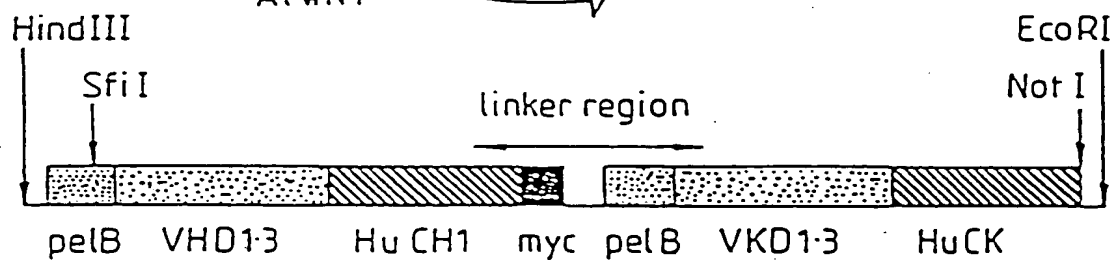


Fig. 48c

← 3' Human CH1 and hinge →
 K P S N T K V D K K V E P K S S T K T H T
 AACCCAGCAACACCAAGGTCGACAAGAAAGTTGAGCCAAATCTTCAACTAAGACGCACACA

→ myc peptide tag →
 S G G E Q K L I S E E D L N * *
 TCAGGAGGTGAACAGAAGCTCATCTCAGAGAGGATCTGAATTAATAAGGGAGCTTGCATGCA

(SEQ ID NO. 263)

← pelB leader →
 M K Y L L P T A A A G L
 AATTCATTTCAAGGAGACAGTCATAATGAATAOCTATTGCCTACGGCAGCCGCTGGATTGT

→ 5' Vk →
 L L P A A Q P A M A D I E L T Q S P
 TATTACCTGCTGCCCAACCAGGATGGGACATGAGTTACCCAGTCTCC

(SEQ ID NO. 264)
 (SEQ ID NO. 265)

Fig.49.

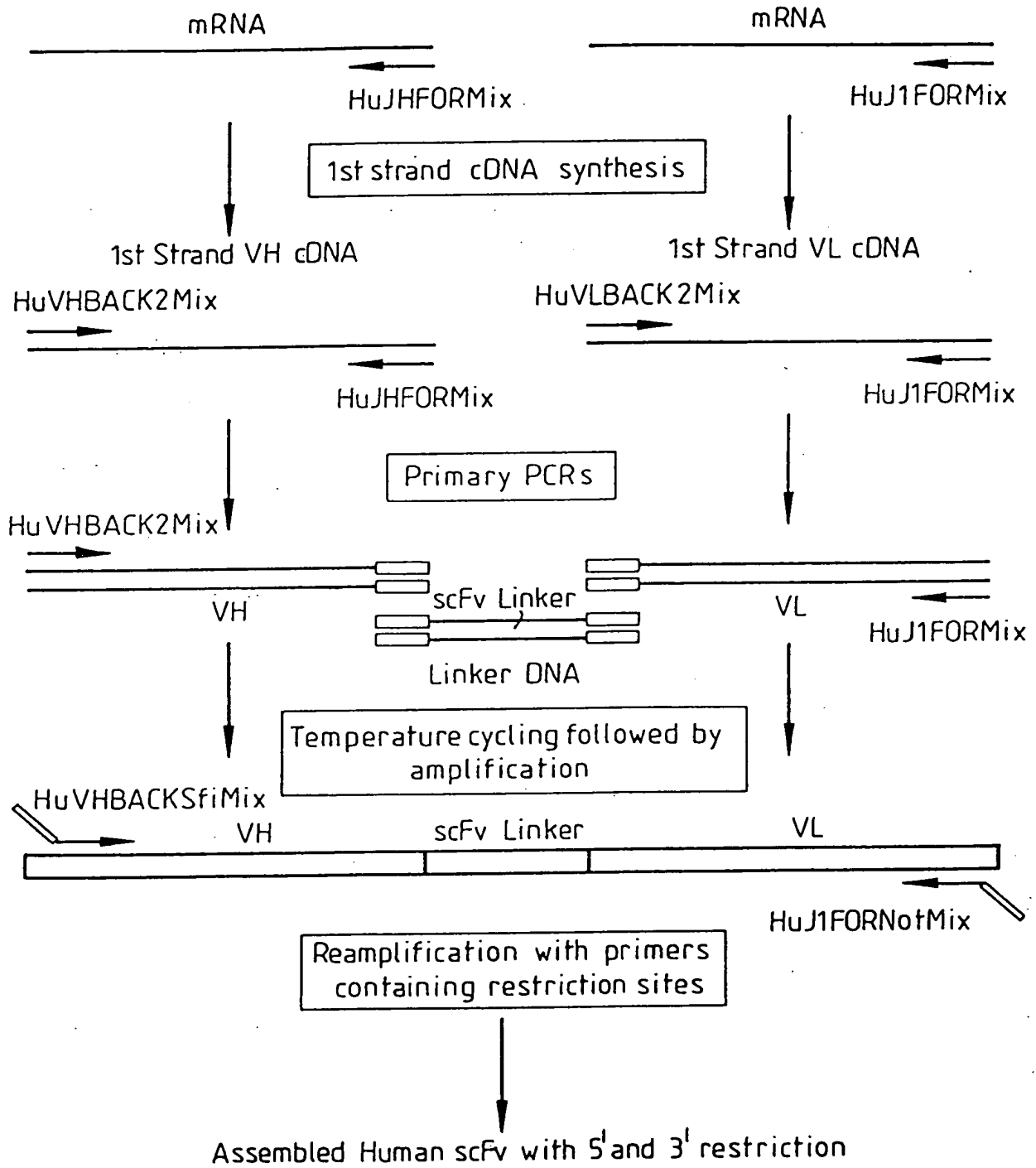


Fig.50a

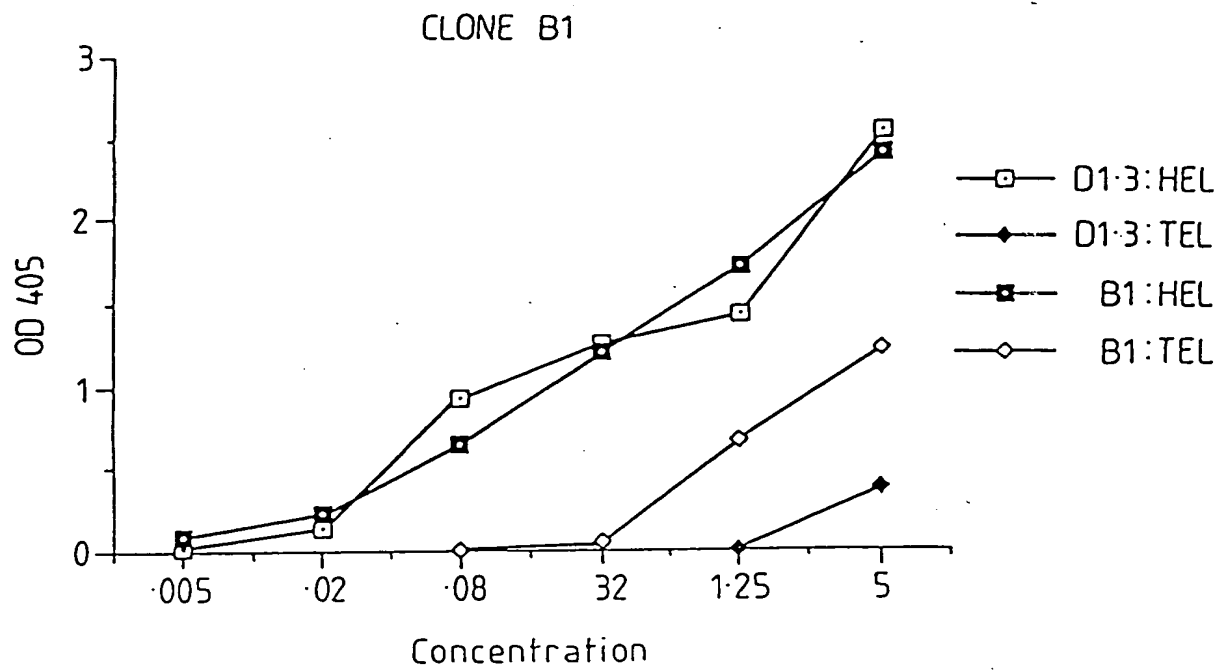


Fig.50b

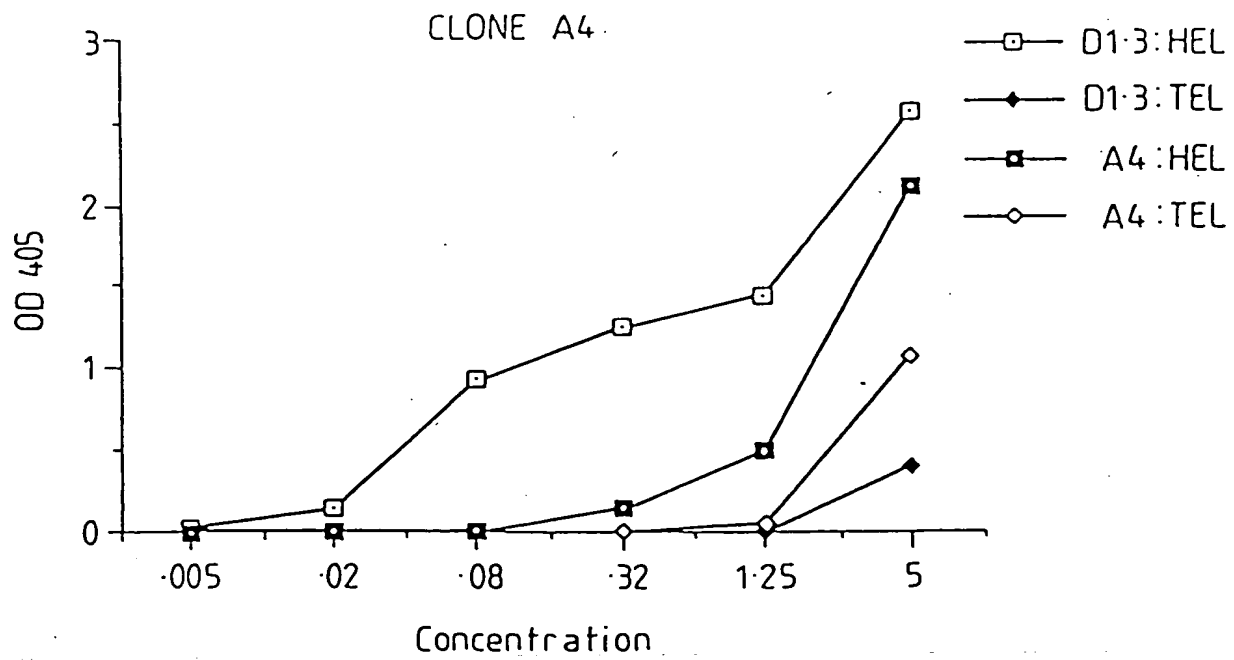


Fig.51.

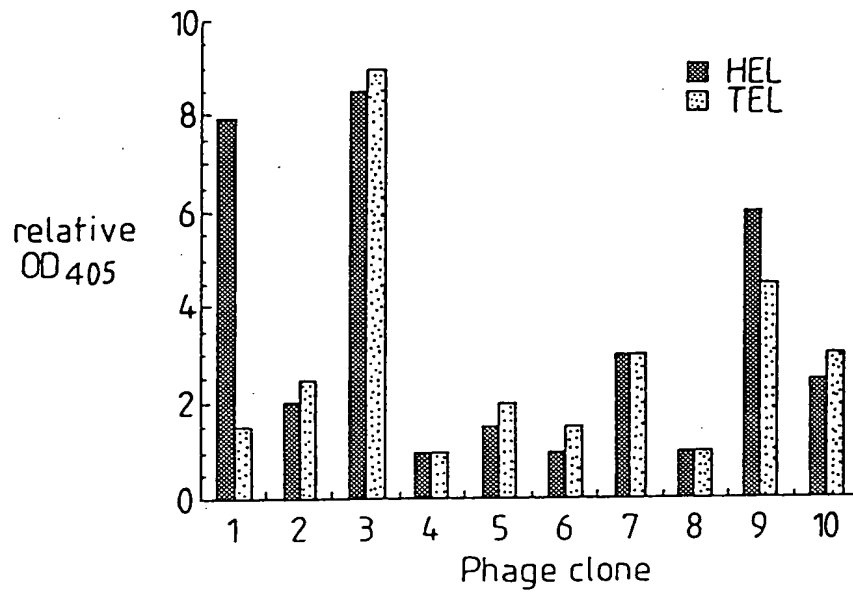


Fig.53.

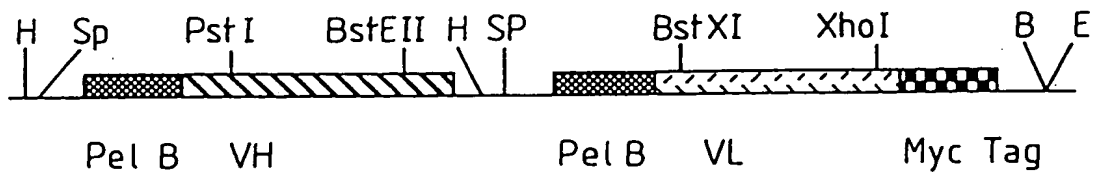


Fig.52.

CDR 1

CDR 2

D1.3 DIQMTQSPASLSASVGETVTITCRASGNIHNYLA WYQQKQKSPQLLVYYTTTLD
M1F DIELTQSPSSLSASLGERVSLTCRASQDIGSSLN WLQQEPDGTIKRLIYATSSLDS
M21 DIELTQSPALMAASPGEKVTITCSVSSSISSSNLHWYQQKSETSPKPWIYGTSNLAS

CDR 3

D1.3 GVPFRFSGSGGTQYSLKINSLQPEDFGSYQCQHFWSPTPTFGGGTKLEIKR
M1F GVPKRFSGSRGSDYSLTISSESEDFVDYVCLQYASSPWTFGGGTKLELKR
M21 GVPVRFSGSGGTSYSLTISSEAEADAATYQCQWSSYPPLTFGAGTKLEIKR